

Tue Jan 20 06:36:39 2004

us-09-955-732-1.rst

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 14:54:29 ; Search time 3778 Seconds
(without alignments)

12737.656 Million cell updates/sec

Title: US-09-955-732-1

Perfect score: 1980

Sequence: 1 atgagccctgcgtacacgtcag.....gagagagagcgagagcctga 1980

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_esc3:*
13: gb_esc4:*
14: gb_esc5:*
15: em_estin:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtl:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_pro:*
24: em_gss_mus:*
25: em_gss_rnd:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 804.6 | 40.6 | 1125 | 12 | BM809903 AGENCOURT |
| 2 | 785 | 39.6 | 991 | 12 | BM471207 AGENCOURT |
| 3 | 783.6 | 39.6 | 1061 | 12 | BM906413 AGENCOURT |
| 4 | 767.2 | 38.7 | 875 | 10 | BM752969 AGENCOURT |

| | | | | | |
|----|-------|------|------|----|---------------------------|
| 5 | 760.6 | 38.4 | 938 | 13 | BU190685 AGENCOURT |
| 6 | 758 | 38.3 | 812 | 10 | BM750408 AGENCOURT |
| 7 | 717.4 | 36.2 | 917 | 13 | BM712114 AGENCOURT |
| 8 | 711 | 35.9 | 750 | 10 | BM511347 AGENCOURT |
| 9 | 706.4 | 35.7 | 947 | 13 | BU537952 AGENCOURT |
| 10 | 706.2 | 35.7 | 790 | 10 | BM326709 AGENCOURT |
| 11 | 698.6 | 35.3 | 846 | 10 | BM563259 AGENCOURT |
| 12 | 674 | 34.0 | 729 | 12 | BM086720 AGENCOURT |
| 13 | 673.8 | 34.0 | 726 | 10 | BM689222 AGENCOURT |
| 14 | 670.8 | 33.9 | 910 | 13 | BM675874 AGENCOURT |
| 15 | 664 | 33.5 | 910 | 10 | BM369297 AGENCOURT |
| 16 | 653.6 | 33.0 | 932 | 10 | BM340220 AGENCOURT |
| 17 | 652.4 | 32.9 | 1004 | 12 | BM910493 AGENCOURT |
| 18 | 641.6 | 32.4 | 919 | 12 | BM737087 AGENCOURT |
| 19 | 639.6 | 32.3 | 790 | 12 | BM008005 AGENCOURT |
| 20 | 639.4 | 32.3 | 931 | 13 | BM6898728 AGENCOURT |
| 21 | 628.8 | 31.7 | 991 | 13 | BM707012 AGENCOURT |
| 22 | 619.8 | 31.3 | 897 | 10 | BM873337 AGENCOURT |
| 23 | 619.2 | 31.3 | 785 | 10 | BM616235 AGENCOURT |
| 24 | 619 | 31.3 | 791 | 10 | BM881145 AGENCOURT |
| 25 | 616.2 | 31.1 | 629 | 12 | BM785529 AGENCOURT |
| 26 | 611.8 | 30.9 | 629 | 12 | BM560192 AGENCOURT |
| 27 | 596 | 30.1 | 1024 | 12 | BM824278 AGENCOURT |
| 28 | 593.4 | 30.0 | 728 | 12 | BM753072 AGENCOURT |
| 29 | 593 | 29.9 | 663 | 10 | BM45391 AGENCOURT |
| 30 | 585.8 | 29.6 | 887 | 14 | BM907514 AGENCOURT |
| 31 | 585.6 | 29.6 | 716 | 10 | BM017302 AGENCOURT |
| 32 | 570.8 | 28.8 | 743 | 12 | BM02806 AL602806 DKEP686L |
| 33 | 569.4 | 28.8 | 721 | 14 | BM166643 IB6603020 |
| 34 | 548.8 | 27.7 | 721 | 14 | BM921565 AGENCOURT |
| 35 | 545.6 | 27.6 | 892 | 12 | BM921421 AGENCOURT |
| 36 | 540.4 | 27.3 | 1228 | 12 | BM831015 AGENCOURT |
| 37 | 540 | 27.2 | 672 | 12 | BM563116 AGENCOURT |
| 38 | 537.6 | 27.2 | 969 | 10 | BM047611 AGENCOURT |
| 39 | 537 | 27.1 | 678 | 12 | BM563401 AGENCOURT |
| 40 | 535.4 | 27.0 | 943 | 12 | BM751542 AGENCOURT |
| 41 | 528.4 | 26.7 | 531 | 10 | BM901875 AGENCOURT |
| 42 | 524 | 26.5 | 890 | 10 | BM898514 AGENCOURT |
| 43 | 510 | 25.8 | 622 | 12 | BM910866 AGENCOURT |
| 44 | 497.8 | 25.1 | 1158 | 12 | BM280203 AGENCOURT |
| 45 | 491 | 24.8 | 599 | 10 | BM280203 AGENCOURT |

ALIGNMENTS

RESULT 1
LOCUS BM809903 1125 bp mRNA EST 05-MAR-2002
DEFINITION AGENCOURT 6581153 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5454822
5' mRNA sequence.

ACCESSION BM809903.1 GI:19126726
VERSION BM809903.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1125)
AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L10M1950 row: 3 column: 07
High quality sequence start: 12

[illegible]

RESULT 3
LOCUS BM906413
DEFINITION
BM906413 1061 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6620017 NIH_MGC_125 Homo sapiens CDNA clone IMAGE:5550371
5', mRNA sequence.
BM906413
BM906413.1 GI:19356792
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1061)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
JOURNAL
AUTHORS
TITLE
COMMENT
Contact: Robert Strausberg, Ph.D.

Email: ccapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L14M12364 row: 5 column: 04
 High quality sequence: scop: 616.
 Location/Qualifiers
 1..1061
 source

| BASE COUNT | 238 a | 344 c | 302 g | 177 e |
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| ORIGIN | | | | |

| | | | | |
|-----------------------|-----------------|---------------------|-----------|--------------|
| Query Match | 39.6% | Score 783.6; | DB 12; | Length 1061; |
| Best Local Similarity | 97.5%; | Pred. No. 1.2e-142; | | |
| Matches 807; | Conservative 0; | Mismatches 19; | Indels 2; | Gaps 1. |

1149 GGAGTCGGCCAGCTGCTGCCGCACTGGAAGGACGCA CGCTTCATTGAGGCTGCAAG 1208

Db 5 GGGATCGGCCAGCTGCTGCCGCACTGGAAGGAGACCGCACCGCTTCATTGAGGCTGCAAG 64

1209 AGCACAGGCGACCCACGCTGCTGCTCCACTGCAGATGGGCGTCAGCCGCTCAGCGGCCAC 126

Db 65 AGCACAGGGCACCACCGTGTGCTCCACTGCAGATGGGGCICAGCCGCTCAGCGCCAC 124

QY 1269 AGTGCCTGGCCATAGCCATGAAAGCAGTACGAAAGCAGCCCTGGAGCAGGCCCTGGCCACCGT 132

[illegible][illegible]

144

304

1448 ATCCCGGAGACGGACCGCCTGAAGTCTTACAACCATTCGCCACTCTCTCCGCAGA 1501

305 CTCCCAGAGGAGCACCAGCCCCCTGAAGTCTCTACACCATTCACCCTCTTCCGCCAGA 364

1509 ACCTGAGGCTGTTGGGAGGAGAAGCTTGTAGGCATGGAAGAGAGCCAGGCAGCCCCGAA 156

Db 365 ACCTGAGGGTGGTGGGAGAGAGGTTGTAGGCATGGAAGAGAGGCCAGGCCCGAA 424

1569 AGAAGACCTGGCCACGGCCACGTATAACCTCCGAGGGTCA TGAGGTCCATCACTCT 162

Db 425 AGAAGAGCCCTGGGCCACGGCCACGTATAACCTCCGAGGGTCATGAGGTCCATCAGTCT 484

1629 TCTGAGCCCTCCTTGAGCTGGAGACACCTCAGAGACCAGTGACATGCCAGAGCTCT 1688

D5 485 TCTGAGCCCTCCTTGAGCTGGAGAGCACCTCAGAGACCAGTGACATGCCAGAGGTC 544

QY 1689 CTCTTCCACGAGTCTTCAATGAGAGCCCTCTGACGCCCTTCCACAGCTTCCAGGAC 1 / 4

Db 545 CTCTTCCACGAGTCTCACATGAAAGCCCTCGACGCCCTCCCAAGCTTCACAGGAC 007

QY 1749 CAAAGGAGGCGCAGAGGTGAGACAGAGGGGCTCAGCCTGAGTCCCGCCAGTCAAGT 1808
 Db 605 CAAAGGAGGCGCAGAGGTGAGACAGAGGGGCTCAGCCTGAGTCCCGCCAGTCAAGT 664
 QY 1809 GGTAACTCTCCAGGAGGAGTCCCTGCTGTCGCAACCGGACCCAGGCTTCCAGAGCAGA 1868
 Db 665 GGTAACTCTCCAGGAGGAGTCCCTGCTGTCGCAACCGGACCCAGGCTTCCAGAGCAGA 724
 QY 1869 GCAAGGGGCGAGGGGCGAGGGGAGAGAGCCCTGATTTCTCTACGCCAGTTCGCG-- 1926
 Db 725 GCAAGGGGCGAGGGGCGAGGGGAGAGAGCCCTGATTTCTCTACGCCAGTTCGCGGA 784
 QY 1927 AAGGTGTGAGACAGGCGCCAGCTGTCATGACAGTGGAGAGAGGCGGAG 1974
 Db 785 AGGTGTGAGACAGGCGCAACGTGTCATGACAGTGGCAAGAGAGGCGG 832

RESULT 4
 LOCUS BG752969 875 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602732427F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4876014 5',
 mRNA sequence.
 ACCESSION BG752969
 VERSION BG752969
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 875)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHCN758 row: e column: 07
 High quality sequence stop: 818.

FEATURES
 source location/Qualifiers
 1..875

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4876014"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_idb="NIH_MGC_43"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."|

BASE COUNT 184 a 267 c 275 g 149 t
 ORIGIN

Query Match 38.7%; Score 767.2; DB 10; Length 875;
 Best Local Similarity 97.0%; Pred. No. 1.7e-139;
 Matches 846; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

QY 196 GAGAGGCCCCGAGTGTAGAGAGGCTCCAGCGGACCCAGACAGACTTGGGCGAGAGATCC 255
 Db 1 GAGAGGCCCCGAGTGTAGAGAGGCTCCAGCGGACCCAGACAGACTTGGGCGAGAGATCC 60

QY 256 CAGAGTCCCAGAAACAGAGAGAGCAGAGGAGCAGCCTGACCTCATGTGTACAGCTGCTG 315
 Db 61 CAGAGTCCCAGAAACAGAGAGAGCAGAGGAGCAGCCTGACCTCATGTGTACAGCTGCTG 120
 QY 316 AGCCCGGAGATGACATCCCGCTGCGAGCCAGCTGAGAGGACCCCGGCTCCCGGCTC 375
 Db 121 AGCCCGGAGATGACATCCCGCTGCGAGCCAGCTGAGAGGACCCCGGCTCCCGGCTC 180
 QY 376 CGCTACCTGTGTAGTATTCTACACAGAAAGAGAGGTGTGAGCCAGATGAGACGGT 435
 Db 181 CGCTACCTGTGTAGTATTCTACACAGAAAGAGAGGTGTGAGCCAGATGAGACGGT 240
 QY 436 CTCTCGGCGGTGAGATTTCCCTGACACAGAGCTCCCCAGCTGCAACCTTGGGCTTGG 495
 Db 241 CTCTCGGCGGTGAGATTTCCCTGACACAGAGCTCCCCAGCTGCAACCTTGGGCTTGG 300
 QY 496 CCCCTCTGAGTGAACACCCAGGTTACTTATGATGAGACGGGGCTTCAGCGTACGCT 555
 Db 301 CCCCTCTGAGTGAACACCCAGGTTACTTATGATGAGACGGGGCTTCAGCGTACGCT 360
 QY 556 GGTGGGCGAAGCCCGATCTTCAAGCCCATCTCCATCCAGACCATGTGGGCGACACTCCAG 615
 Db 361 GGTGGGCGAAGCCCGATCTTCAAGCCCATCTCCATCCAGACCATGTGGGCGACACTCCAG 420
 QY 616 GTATTGACACCAAGCATGTGAGGAGCCTCTAGGAGCGGCGCTTGTACCGGGTGGCAGTGC 675
 Db 421 GTATTGACACCAAGCATGTGAGGAGCCTCTAGGAGCGGCGCTTGTACCGGGTGGCAGTGC 480
 QY 676 CTCACTTGGGCGACCCACTACACAGAGAGACTGAATCTCCAGACAGAGCTCTCAATAG 735
 Db 481 CTCACTTGGGCGACCCACTACACAGAGAGACTGAATCTCCAGACAGAGCTCTCAATAG 540
 QY 736 TGGAGCGGTATGCGCGACCTGAGAGTCTCTCGGCGCTCCGACCGGCGCTGGCGGCTGC 795
 Db 541 TGGAGCGGTATGCGCGACCTGAGAGTCTCTCGGCGCTCCGACCGGCGCTGGCGGCTGC 600
 QY 796 TCAGACAGAGACAGATGAGAGCAGCGCATCTGCTGAGCTGTGAGAAAGTGTGATGTC 855
 Db 601 TCAGACAGAGACAGATGAGAGCAGCGCATCTGCTGAGCTGTGAGAAAGTGTGATGTC 660
 QY 856 AGTACCTTGA-GAGTGTCACTTCCAAAGAGATCCGCAAGCTCTGAGAGTGGCGCTGGG 914
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 QY 915 GCTCCCCC-TCAGACAGTACCGTGACTTCAATGACAAC--AGATGCTCTCTGATGG 970
 Db 721 GCTCCCCCCTTCAGACATACCGTGACTTCAATGACAACAGATGCTCTGATGG 780
 QY 971 CACAGCGGAGCCGAGCTCTCCGATCTTCCCACTCTACTGAGGCTCAGAGTGAAG 1030
 Db 781 CACAGCGGAGCCGAGCTCTCCG-ATCTTCCCACTCTACTGAGTGGG-TCAGAGTGAAG 838
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 Db 839 CAG-AAACTTGAAGAGCTCCAGAGAACAG 869

RESULT 5 938 bp mRNA linear EST 04-SEP-2002
 BUI90685
 LOCUS AGENCOURT_7953319 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:6107345
 DEFINITION 5', mRNA sequence.
 ACCESSION BUI90685
 VERSION BUI90685
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 938)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished

[illegible]

| | |
|------------|--|
| RESULT | 7 |
| LOCUS | BQ712114 |
| DEFINITION | BQ712114 917 bp MRNA linear EST 16-JUL-2002 |
| ACCESSION | AGNCNCURT_8418352 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:62817228 |
| VERSION | 5, mRNA sequence. |
| KEYWORDS | BQ712114 BQ712114.1 GI:21851013 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 917) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strusberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson |

CDNA Library Preparation Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LCC2474 row: p column: 15
High quality sequence stop: 584.
Location/Qualifiers
1..517
FEATURES
source

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/clone="IMAGE:6281726"
/lab_host="RDH10B (phage-resistant)"
/clone_id="NIH_MGC_113"
/notes="Organ: spleen; Vector: pCIB7; Site_1: XhoI; Site 2
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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| Query Match | 36.2% | Score 717.4 | DB 13 | Length 917 |
|-----------------------|--------------|--|------------|------------|
| Best Local Similarity | 99.2% | Pred. No. 9e-130 | | |
| Matches 721 | Conservative | 0 | Mismatches | 6 |
| | | | Indels | 0 |
| | | | Gaps | 0 |
| QY | 1254 | CCGCTCAGCGGCACACAGTCTGGCTTATGCCATGAAAGCACTACGAATGCAGCTTGAGACA | 1311 | |
| DB | 1 | CCGCTCAGCGGCACACAGTCTGGCTTATGCCATGAAAGCACTACGAATGCAGCTTGAGACA | 60 | |
| QY | 1314 | GGCCCTGCGCCACGTCGAGAGACTCCGGCCCATGCGCCGCCAACCTTGGCTTCTCGG | 1372 | |
| DB | 61 | GGCCCTGCGCCACGTCGAGAGACTCCGGCCCATGCGCCGCCAACCTTGGCTTCTCGG | 120 | |
| QY | 1374 | CCAGCTGCAGATCTTACCAAGGCAATCTTGAACGCGCAGCCGACAGGCAATGTCTGGAGACA | 1433 | |
| DB | 121 | CCAGCTGCAGATCTTACCAAGGCAATCTTGAACGCGCAGCCGACAGGCAATGTCTGGAGACA | 180 | |
| QY | 1434 | GAAATGGAGTGGGGTCTCCACAGAGAGACCCAGCCCTGGAAGTCTTACACCAATTTCCC | 1493 | |
| DB | 181 | GAAATGGAGTGGGGTCTCCACAGAGAGACCCAGCCCTGGAAGTCTTACACCAATTTCCC | 240 | |
| QY | 1494 | ACCTTTTCCGCAAGAACTTGAAGGTGTGGGGAGAGAAAGTTTATGCGATGAAAGAGAG | 1555 | |
| DB | 241 | ACCTTTTCCGCAAGAACTTGAAGGTGTGGGGAGAGAAAGTTTATGCGATGAAAGAGAG | 300 | |
| QY | 1554 | CCAGGACAGCCCGAAAGAGAGAGCTGGGGCCACGGCCACGATTTAAACTCTCCAGAGGGTAT | 1613 | |
| DB | 301 | CCAGGACAGCCCGAAAGAGAGAGCTGGGGCCACGGCCACGATTTAAACTCTCCAGAGGGTAT | 360 | |
| QY | 1614 | GAGGTCCATCACTTTCTTGAAGCTCTTGAAGCTTGAAGAGCACTCAGAGACCACTGTA | 1673 | |
| DB | 361 | GAGGTCCATCACTTTCTTGAAGCTCTTGAAGCTTGAAGAGCACTCAGAGACCACTGTA | 420 | |
| QY | 1674 | CATGCAAGAGTCTTCTCTTCCACAGAGTCTTCACTAATGAAGAGCTCTGCAGCCCTTCC | 1733 | |
| DB | 421 | CATGCAAGAGTCTTCTCTTCCACAGAGTCTTCACTAATGAAGAGCTCTGCAGCCCTTCC | 480 | |
| QY | 1734 | ACAAGTTCAGAGACCAAGGAGGCGCAGCAGGTGAGCAGGGGGCTCAGCTGCCCTGTA | 1799 | |
| DB | 481 | ACAAGTTCAGAGACCAAGGAGGCGCAGCAGGTGAGCAGGGGGCTCAGCTGCCCTGTA | 540 | |
| QY | 1794 | GTCGCGCAGATCAATGTGTATACCTTCCAGGGCAGATGCGGTGTGGCCAAACCGAACCAAGC | 1855 | |
| DB | 541 | GTCGCGCAGATCAATGTGTATACCTTCCAGGGCAGATGCGGTGTGGCCAAACCGAACCAAGC | 600 | |
| QY | 1854 | CTTCAGAGACGAGAGCAGGGGCGCAGGGGCGAGGGGCGAGGGAGGCTTGATTTCTCTTAC | 1919 | |

| | | | | |
|----|---------------------------|---|---|-----------------------------|
| Db | | 601 | CTTCCAGACGACGAGCAGGGCGCACGGGGCAGGGGCAGAGAGACCCTCGATTTCCTCAAC | 660 |
| Qy | | 1914 | GCCCCAGGTTCGCCGAAGTGTTGTAACAAGCCACGCGTAGCATGATGATGAGAGAGAGGCCA | 1973 |
| Dd | | 661 | GCCCAGGTTCCGGAAGGTGTGTAGAACAAGCCAGCGTAGTCATGATGAAACTGGAAGGAGGCG | 720 |
| Qy | | 1974 | GCGCTGA | 1980 |
| Db | | 721 | AGCCTGA | 727 |
| | RESULT 8 | | | |
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| | DEFINITION | 601278540rl NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610616 5' | | |
| | ACCESSION | BES31347 | | |
| | VERSION | BES31347.1 GI:9759906 | | |
| | KEYWORDS | EST. | | |
| | SOURCE | Homo sapiens (human) | | |
| | ORGANISM | Homo sapiens | | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| | REFERENCE | NIH-MGC http://mgc.nci.nih.gov/. | | |
| | AUTHORS | 1 (bases 1 to 750) | | |
| | TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| | JOURNAL | Unpublished | | |
| | COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: http://image.lnl.gov Plate: LINC266 row: p column: 09 High quality sequence start: 3 High quality sequence stop: 750. Location/Qualifiers | | |
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| | | /clone="IMAGE:3610616" | | |
| | | /tissue.type="adenocarcinoma" | | |
| | | /lab_host="DH10B (phage-resistant)" | | |
| | | /clone.lib="NIH MGC 39" | | |
| | | /note="Organ: pancreas; Vector: pCMV7; Site 1: XhoI; Site 2: EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." | | |
| | BASE COUNT | 158 a 240 c 252 g 120 t | | |
| | ORIGIN | | | |
| | Query Match | 35.9%; Score 711; DB 10; Length 750; | | |
| | Best Local Similarity | 100.0%; Pred. No. 1.5e-18; | | |
| | Matches 711; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | |
| Qy | | 1100 | ACTTTACACCTGAGCGCTTCACTTACACAAATGTCGCGCTCGGATAGAGAGTGCGCC | 1159 |
| Dd | | 40 | ACTTTCACCTGAGCGCTTCACTTACACAAATGTCGCGCTCGGATAGAGAGTGCGCC | 99 |
| Qy | | 1160 | AGCTGCGCGGCACTGGAAGAGAACCCACCGCTTACATTAGAGCTGCAGAGACAGGCA | 1219 |
| Dd | | 100 | AGCTGCTCGCGCACTGGAAGAGAACCCACCGCTTACATTAGAGCTGCAGAGACAGGCA | 159 |
| Qy | | 1220 | CACAGTGTGTCTCACTGCAAGATGGGGTCAAGCGCTCAAGGGCCACAGTGTGGGCT | 1279 |

| | | | | | |
|------------|--|--|------|--|------|
| D | b | | 160 | CCCACTGCTGTGCCTCAGTCCAGAAATGGGGGTACAGCCGCTCAGAGGCCAACAAGTGCTGGCT | 219 |
| Q | y | | 1280 | ATGCCATGAAGCAGTAACGAATGCAATGCAAGCTTGAAGTAGAGCCCTTCGGCCACTCGTAGAGAGCTCC | 1339 |
| D | b | | 220 | ATGCCATGAAGCAGTACGAATGCAAGCTTGAAGTAGAGCCCTTCGGCCACTCGTAGAGAGCTCC | 279 |
| Q | y | | 1340 | GGGCCATCGGCCCCCAACCCTGGCTTCTCTGGCCAGCTGCAGATCTAACAGGGCATCC | 1399 |
| D | b | | 280 | GGCCCATTCGCCGCCCCCMAACCTTGCTTCTTGCCACAGCTGCAGATCTAACAGGGCATCC | 339 |
| Q | y | | 1400 | TGACGGCCAGCCGCCAGAGCCATGTCTGGAGCAGAAAGTGGGTGGGTCTCCCCAGAG | 1459 |
| D | b | | 340 | TGACGGCCAGCCGCCAGAGCCATGTCTGGAGCAGAAAGTGGGTGGGTCTCCCCAGAG | 399 |
| Q | y | | 1460 | AGCACCCAGCCCTGAAAGTTCTACACCAATCCCACTCTTCGGCCAGAATCTGAGGGT | 1519 |
| D | b | | 400 | AGCACCCAGCCCTGAAAGTTCTACACCAATCCCACTCTTCGGCCAGAATCTGAGGGT | 459 |
| Q | y | | 1520 | GTCGGGAGAGAAAGTTGTAGGCATGGAGAGACCAAGCAGCCCGGAAAAGAGCTTG | 1579 |
| D | b | | 460 | GTCGGGAGAGAAAGTTGTAGGCATGGAGAGACCAAGCAGCCCGGAAAAGAGCTTG | 519 |
| Q | y | | 1580 | GGCCACGGCCACGTATTAAACCTCCAGGGGTCAATGAGTCATCAGTCTTCTGAGCCT | 1639 |
| D | b | | 520 | GGCCACGGCCACGTATTAAACCTCCAGGGGTCAATGAGTCATCAGTCTTCTGAGCCT | 579 |
| Q | y | | 1640 | CCTTGAGCTGAGAGCAGCCTCAGAGACCAAGTGCATGACAGAGTCTTCTTCCACG | 1699 |
| D | b | | 580 | CCTTGAGCTGAGAGCAGCCTCAGAGACCAAGTGCATGACAGAGTCTTCTTCCACG | 639 |
| Q | y | | 1700 | AGTCTTCACTGAAGAACCTCTGAGGCCCTCCACAGCTTGCAAGGACCAAGGGAGGCC | 1759 |
| D | b | | 640 | AGTCTTCACTGAAGAACCTCTGAGGCCCTCCACAGCTTGCAAGGACCAAGGGAGGCC | 699 |
| Q | y | | 1760 | AGCAGGTGAGACAGGGGGCTCAGCCTCCCTGAAAGTCCCGCACTAGTGG | 1810 |
| D | b | | 700 | AGCAGGTGAGACAGGGGGCTCAGCCTCCCTGAAAGTCCCGCACTAGTGG | 750 |
| RESULT 9 | BUS37952 | | | | |
| LOCUS | | | | | |
| DEFINITION | AGENCOURT 10186579 NIH MGC 107 Homo sapiens cDNA clone | | | | |
| ACCESSION | BUS37952 | | | | |
| VERSION | BUS37952.1 | | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| TITLE | 1 (bases 1 to 947) | | | | |
| JOURNAL | NIH-MGC http://mgs.nci.nih.gov/. | | | | |
| COMMENT | National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cga@bs-remail.nih.gov Tissue procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN). DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: L1CM2754 row: c column: 17 High quality sequence stop: 614. Location/Qualifiers 1..947 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6568457" /tissue_type="adenocarcinoma, cell line" | | | | |


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Db      410 CGGCTCCCGGCTCCGCTACCTGCTGTAGTTTCTTACACGAGAGGAGAGGCTGTAGC 469
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Qy      601 TGGGCGACACTCCAGGATTTGACAC-AGCATGTGAGGAGGAGCTTAAAGGAGCGGCTTGT 659
Db      650 TGGGCGACACTCCAGGATTTGACAC-AGCATGTGAGGAGGAGCTTAAAGGAGCGGCTTGT 709
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DEFINITION mRNA sequence.
ACCESSION BE563259
VERSION BE563259.1 GI:9807071
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 846)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHM384 row: a column: 18
High quality sequence stop: 709.
Location/Qualifiers
1. 846

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FEATURES

source

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/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
BASE COUNT 172 a 252 c 266 g 156 t

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ORIGIN

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Query Match 35.3%; Score 698.6; DB 10; Length 846;
Best Local Similarity 96.9%; Pred. No. 4.1e-126;
Matches 776; Conservative 0; Mismatches 19; Indels 6; Gaps 6;

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RESULT 12

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VERSION B1086720.1 GI:14505050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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ACCESSION BG169297
VERSION BG169297.1 GI:12676000
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 910)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0167 row: f column: 07
High quality sequence stop: 742.
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/mol_type="mRNA"
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/clone_lib="NIH_MGC_89"
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 189 a 270 c 304 g 146 t 1 others
ORIGIN
Query Match 33.5%; Score 664; DB 10; Length 910;
Best Local Similarity 95.7%; Pred. No. 2.3e-119;
Matches 757; Conservative 0; Mismatches 26; Indels 8; Gaps 7;
QY 534 CGGGGGCTTCAGCGTGTGAGGCGCAAGCCGATCTTCAAGCCCATCTCCATCCA 593
DB 1 CGGGGGCTTCAGCGTGTGAGGCGCAAGCCGATCTTCAAGCCCATCTCCATCCA 60
QY 594 GACCATGTGGGCGACATCTCAGGTATTGACCAAGCATGTGAGCGAGCTTAGGCGCG 653
DB 61 GACCATGTGGGCGACATCTCAGGTATTGACCAAGCATGTGAGCGAGCTTAGGCGCG 119
QY 654 CCTTGTACCGGGGTGGAGTGGCCCTCACTGGGGCGACGATACGAGAGAGATGAACTC 713
DB 120 CCTTGTACCGGGGTGGAGTGGCCCTCACTGGGGCGACGATACGAGAGAGATGAACTC 179
QY 714 CGAACAAGACTCTCTCAATGATGAGCGGCTATGGCCGACTGAGTCTTGGGCTCC 773
DB 180 CGAACAAGACTCTCTCAATGATGAGCGGCTATGGCCGACTGAGTCTTGGGCTCC 239
QY 774 CAGCGCGAGCTGGGGGTCTCTCAAGACAGAGAGATGAGAGAGGATCCGTGTA 833
DB 240 CAGCGCGAGCTGGGGGTCTCTCAAGACAGAGAGATGAGAGAGGATCCGTGTA 299
QY 834 GCTGTGAAAGTGTGATGTCACTGAGAGTGTCACTTCCAAGAGATCCGCCA 893
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QY 894 GGGCTGTGAGCTGGCGCTGGGGCTCCCTCCAGCATACCTGACTTCATGACACCA 953
DB 359 GGGCTGTGAGCTGGCGCTGGGGCTCCCTCCAGCATACCTGACTTCATGACACCA 418

QY 954 GATGCTGCTCTGTGTGACACAGCGGACCGAGCTCCCGCATCTTCCCGACCTTAACCT 1013
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QY 1014 GGGCTAGATGGAACGACCAAACTGAGAGCTGACAGAGGAACAGGGTCAACCCACAT 1073
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DB 774 GCGCTGCGCAC 784

Search completed: January 15, 2004, 18:29:18
Job time : 3788 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 13:11:13 ; Search time 532 Seconds

(without alignments)
10046.781 Million cell updates/sec

Title: US-09-955-732-1

Perfect score: 1980
Sequence: 1 atggccctgcagcagctgag.....gagagagagcgcagcctga 1980

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1980 | 100.0 | 2718 | 24 | AA036061 Human dual-specific |
| 2 | 1978.4 | 99.9 | 2781 | 22 | AA030485 Human protein phos |
| 3 | 1978.4 | 99.9 | 2852 | 24 | AB073250 Human MAP kinase P |
| 4 | 1774 | 89.6 | 2618 | 24 | AA036063 Murine dual-specific |
| 5 | 1774 | 89.6 | 2704 | 24 | AB073249 Human MAP kinase P |
| 6 | 1774 | 89.6 | 2704 | 24 | AB073252 Human MAP kinase P |
| 7 | 1684 | 85.1 | 2322 | 24 | AB040805 Human MAP kinase P |
| 8 | 1345.6 | 68.0 | 2540 | 24 | AB073251 Human MAP kinase P |

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|----|-------|------|------|----|------------------------------|
| 9 | 1026 | 51.8 | 1026 | 22 | AA063578 Human phosphatase |
| 10 | 851 | 43.0 | 2061 | 24 | AEN59832 Novel human coding |
| 11 | 694 | 35.1 | 1755 | 22 | AA044722 Human cDNA sequenc |
| 12 | 694 | 35.1 | 1755 | 24 | AB040801 Human MAP kinase P |
| 13 | 491 | 24.8 | 599 | 24 | AB040803 Human MAP kinase P |
| 14 | 397 | 20.1 | 409 | 24 | AB040802 Human MAP kinase P |
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| 16 | 362 | 18.3 | 6374 | 22 | AA094911 Human GSP006 phosp |
| 17 | 356.4 | 18.0 | 494 | 24 | AB040804 Human MAP kinase P |
| 18 | 340.4 | 17.2 | 1949 | 22 | AD029655 Human dual-specific |
| 19 | 325 | 16.6 | 426 | 24 | AB040800 Human MAP kinase P |
| 20 | 308.8 | 15.6 | 1711 | 22 | AD012966 Human dual-specific |
| 21 | 300.8 | 15.2 | 3488 | 24 | AB057466 Human protein phos |
| 22 | 293.6 | 14.8 | 4467 | 23 | AB010739 Drosophila melanog |
| 23 | 282.8 | 14.3 | 2260 | 22 | AD094933 Human GSP001 phosp |
| 24 | 279.4 | 14.1 | 1771 | 22 | AA022966 Human phosphatase |
| 25 | 278 | 14.0 | 1348 | 22 | AA099712 Human protein enco |
| 26 | 233.4 | 11.8 | 571 | 22 | AA070577 Human cDNA clone |
| 27 | 204 | 10.3 | 1052 | 22 | AD012967 Human dual-specific |
| 28 | 163.4 | 8.3 | 969 | 22 | AA059843 Human novel cyclin |
| 29 | 163 | 8.2 | 5029 | 25 | ABX34583 Human mdt cDNA SE |
| 30 | 156.6 | 7.9 | 1450 | 22 | AA041387 cDNA encoding nove |
| 31 | 156.6 | 7.9 | 1450 | 22 | AA034834 Drosophila melanog |
| 32 | 142 | 7.2 | 8002 | 23 | AB010738 Human ORFX ORF620 |
| 33 | 123.2 | 6.2 | 447 | 21 | AA075065 Human cDNA encodin |
| 34 | 101.8 | 5.1 | 1390 | 22 | AA012700 Human KPP-1 cDNA, |
| 35 | 101.8 | 5.1 | 1605 | 25 | ABA00716 Human protein phos |
| 36 | 98.8 | 5.0 | 1236 | 24 | AA024021 Human ovarian anti |
| 37 | 98.8 | 5.0 | 1357 | 24 | AB050303 Human activated T |
| 38 | 98.8 | 5.0 | 1685 | 25 | ABX62935 Human cDNA differe |
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| 40 | 98.8 | 5.0 | 1710 | 25 | ABX10959 Human phosphatase |
| 41 | 93.8 | 4.7 | 687 | 22 | AA063575 Human dual specific |
| 42 | 89.2 | 4.5 | 2139 | 25 | ABX09053 Human DNA sequence |
| 43 | 89.2 | 4.5 | 2400 | 24 | AA034769 Human dual specific |
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| 45 | 88 | 4.4 | 1435 | 25 | AB074143 Human dual specific |

ALIGNMENTS

RESULT 1
ID AAD36061 standard; cDNA; 2718 BP.

XX AAD36061;

XX 09-AUG-2002 (first entry)

DE Human dual-specificity phosphatase 15 (DSP-15) cDNA.

XX Human; dual-specificity phosphatase 15; DSP-15; antiallergic; cytosolic;

KW immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;

KW signal transduction; cell proliferation; Duchenne muscular dystrophy;

KW cell cycle abnormality; graft-versus-host disease; autoimmune disease;

KW metabolic disease; allergy; screening; chromosome 11q; gene; ss.

OS Homo sapiens.

XX Key

XX CDS

XX 19-SEP-2001; 2001WO-US29406.

XX 19-SEP-2000; 2000US-23833P.

PR 18-SEP-2001; 2001US-0955732.

Location/Qualifiers
/tag= a
/product= "Human DSP-15 protein"

XX (CEPT-) CEPTYR INC.
 PA Luche RM, Wei B;
 XX WPI: 2002-394127/42.
 XX P-PSPB; AAE22729.
 DR New dual-specificity phosphatase 15 polypeptide and polynucleotides,
 XX useful for treating e.g. Duchenne muscular dystrophy, cancer,
 PT graft-versus-host disease, autoimmune diseases, allergies, metabolic
 PT diseases
 XX
 PS Claim 7, Fig 1, 91pp; English.
 CC The invention relates to a new isolated dual-specificity phosphatase 15
 CC (DSP-15) polypeptide which retains the ability to dephosphorylate an
 CC activated MAP (mitogen activated protein) kinase. DSPs are phosphatases
 CC that dephosphorylate both phosphotyrosine and phosphoserine/serine
 CC residues. DSP-15 polypeptides may be used to identify agents that
 CC modulate DSP-15 activity, where such agents may inhibit or enhance signal
 CC transduction via a MAP-kinase cascade, leading to cell proliferation. DSP
 CC polypeptides, modulating agents, and/or polynucleotides encoding the
 CC polypeptides may be used to modulate DSP-15 activity in a patient, and to
 CC ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft-
 CC versus-host disease, autoimmune diseases, allergies, metabolic diseases,
 CC abnormal cell growth, abnormal cell proliferation and cell cycle
 CC abnormalities. DSP-15 alternate form polypeptides are useful in screening
 CC assays for modulators of enzyme activity and/or substrate binding. The
 CC present sequence is human DSP-15 cDNA. Human DSP-15 gene is located on
 CC chromosome 11q.
 XX
 SQ Sequence 2718 BP; 559 A; 893 C; 795 G; 471 T; 0 other;
 Query Match 100.0%; Score 1980; DB 24; Length 2718;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 541 TTCAAGCGTACGCTCTGGTGGGCAAAAGCCGATCTTCAAGCCCATCTCCATCCAGACCATG 600
 DB 575 TTCAAGCGTACGCTCTGGTGGGCAAAAGCCGATCTTCAAGCCCATCTCCATCCAGACCATG 634
 QY 601 TGGGCAACACTCCAGATTTGACCAAGCACTGTGAGCAGCTCTAGGACAGCGGCTTGTA 660
 DB 635 TGGGCAACACTCCAGATTTGACCAAGCACTGTGAGCAGCTCTAGGACAGCGGCTTGTA 694
 QY 661 CCGGATGACAGTCCCTCCAGCTGGGACGACCACTTACAGAGAGACTGAACTCCGAAAG 720
 DB 695 CCGGATGACAGTCCCTCCAGCTGGGACGACCACTTACAGAGAGACTGAACTCCGAAAG 754
 QY 721 AGCTGCTCAATGATGATGACGAGCTATGAGCCGACCTGAGTCTGCGGCGCTCCAGCGCC 780
 DB 755 AGCTGCTCAATGATGATGACGAGCTATGAGCCGACCTGAGTCTGCGGCGCTCCAGCGCC 814
 QY 781 GAGCTGCGGAGTCTCCAGAAACAGAGACAGATGAGAGAGGAGTCCGCTGAGAGCTGG 840
 DB 815 GAGCTGCGGAGTCTCCAGAAACAGAGACAGATGAGAGAGGAGTCCGCTGAGAGCTGG 874
 QY 841 AAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 DB 875 AAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 934
 QY 901 GAGCTGCGGAGTCTCCAGAAACAGAGACAGATGAGAGAGGAGTCCGCTGAGAGCTGG 960
 DB 935 GAGCTGCGGAGTCTCCAGAAACAGAGACAGATGAGAGAGGAGTCCGCTGAGAGCTGG 994
 QY 961 CTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 DB 995 CTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1054
 QY 1021 GAGTGAACAGGAGAACTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1055 GAGTGAACAGGAGAACTGAG 1114
 QY 1081 ATGACCCGAGAGATTTGAACTTCTACCTGAGCGCTTCACTTACCAAGATGAGCTTC 1140
 DB 1115 ATGACCCGAGAGATTTGAACTTCTACCTGAGCGCTTCACTTACCAAGATGAGCTTC 1174
 QY 1141 TGGATGAGAGAGTGGGCGGAGCTGCTGCGGCACTGGAAGAGAGAGAGAGAGAGAGAG 1200
 DB 1175 TGGATGAGAGAGTGGGCGGAGCTGCTGCGGCACTGGAAGAGAGAGAGAGAGAGAGAG 1234
 QY 1201 GCTGCAAG 1260
 DB 1235 GCTGCAAG 1294
 QY 1261 GCGGCAAG 1320
 DB 1295 GCGGCAAG 1354
 QY 1321 GCGGCAAG 1380
 DB 1355 GCGGCAAG 1414
 QY 1381 CAGATCTACAG 1440
 DB 1415 CAGATCTACAG 1474
 QY 1441 GGTGGGAGTCTCCAG 1500
 DB 1475 GGTGGGAGTCTCCAG 1534
 QY 1501 CCGCAGAAACCTGAG 1560
 DB 1535 CCGCAGAAACCTGAG 1594
 QY 1561 GCGCCGAAAG 1620
 DB 1595 GCGCCGAAAG 1654

| | | | | |
|----------|--------------|--|---|-----|
| Oy | | 1621 | ATCAGTCTTCCTGGACCCCTCCCTTGAGGCTGGAGAGCACTCGAAGACCAGTAGCATGCCA | 168 |
| Dd | | 1655 | ATCATGTCTTCCTGGACCCCTCCTTGSAGCTGGAGAGCACTCGAGAACAATGATGCCA | 171 |
| Oy | | 1661 | GAGGTCTTCCTCTCCACAGACTCTTCAATGAAAGGCTCTTGAGCCCTTCCACAGCTT | 174 |
| Dd | | 1745 | GAGGTCTTCCTCTCCACAGACTCTTCAATGAAGAGCCCTCTGCAAGCCCTTCCACAGCTT | 177 |
| Oy | | 1741 | GCAAGGACCAAGAGGAGGCGCAGAGGTGACAGAGGGGGCTCAAGCTGCCTGAAAGTCCCGC | 180 |
| Dd | | 1775 | GCAAGGACCAAGAGGAGGCGCAGAGGTGACAGAGGGGGCTCAAGCTGCCTGAAAGTCCCGC | 183 |
| Oy | | 1801 | CAGTCAGTGTATTACCTCCACAGGGCAGTGGCCGTGTGGCCAACGGACCCAGGCTTTCCAG | 186 |
| Dd | | 1835 | CAGTCAGTGTATTACCTCCACAGGGCAGTGGCCGTGTGGCCAACGGACCCAGGCTTTCCAG | 189 |
| Oy | | 1861 | GAGCAGGAGCACAGGGGCGAGGGGCGAGGGAGAGCCCTGATTTCTCTTAAGCCCAAG | 192 |
| Dd | | 1895 | GAGCAGGAGCACAGGGGCGAGGGGCGAGGGAGAGCCCTGATTTCTCTTAAGCCCAAG | 195 |
| Oy | | 1921 | TTCGGGAAGGTGTGTAGACAGAGCCAGCGTGATGACAGTGGAGAGAGGAGCGAGGCTGTA | 198 |
| Dd | | 1955 | TTCGGGAAGGTGTGTAGACAGAGCCAGCGTGATGACAGTGGAGAGAGGAGCGAGGCTGTA | 201 |
| <hr/> | | | | |
| RESULT 2 | | | | |
| XX | ID | AAF30485 | AAF30485 standard; cDNA; 2781 BP. | |
| XX | AC | AAF30485; | | |
| XX | DT | 29-MAY-2001 | (first entry) | |
| DE | XX | Human protein phosphatase and kinase protein-10 cDNA 5039718CBL. | | |
| KM | XX | Protein phosphatase and kinase protein; pPMP-10; human; | | |
| KM | XX | gastrointestinal disorder; immune system disorder; | | |
| KM | XX | neurological disorder; cell proliferative disorder; cancer; | | |
| KM | XX | diagnosis; therapy; ss. | | |
| OS | XX | Homo sapiens. | | |
| FT | Key | Location/Qualifiers | | |
| FT | CDS | 87..2066 | | |
| FT | | /tag= a | | |
| FT | sig_peptide | 87..143 | | |
| FT | | /tag= b | | |
| FT | mat_peptide | 144..2063 | | |
| FT | | /tag= c | | |
| FT | misc_feature | 219..279 | | |
| FT | | /tag= d | | |
| FT | misc_feature | /note= "unique fragment" | | |
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| FT | | /tag= e | | |
| FT | | /note= "unique fragment" | | |
| <hr/> | | | | |
| XX | PN | WO200120004-A2. | | |
| XX | PD | 22-MAR-2001. | | |
| XX | PF | 14-SEP-2000; 2000WO-US25515. | | |
| XX | PR | 15-SEP-1999; 99US-0154141. | | |
| XX | RA | (INCY-) INCYTE GENOMICS INC. | | |
| XX | PI | Yue H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y, | | |
| XX | Pt | Lu DAM; | | |
| XX | WP | WPI: 2001-244811/25. | | |
| XX | DR | P-PDB; AAB20331. | | |
| XX | TX | Novel human protein phosphatase and kinase proteins for diagnosis, | | |

| Query Match | Best Local Similarity | 99.9% | Score 1978.4 | DB 22 | Length 2781 |
|--------------|-----------------------|---|--------------|--------------|-------------|
| Matches 1979 | Conservative | 99.9% | Pred. No. 0 | Mismatches 1 | Indels 0 |
| | | | | Gaps 0 | |
| QY | 1 | ATGAGCCTGTGTCACAGATGAGCCGTTTCGCCCCCGGAGCGCGCTCCACGCGCCTGCGG | 60 | | |
| DB | 87 | ATGAGCCTGTGTCACAGATGAGCCGTTTCGCCCCCGGAGCGCGCTCCACGCGCCTGCGG | 146 | | |
| QY | 61 | CCCGTGGGACACAGGGGGGTCCACGAGAGAGTGATGCTCCAGCGCAAGGACAGAGCTTTCGGG | 120 | | |
| DB | 147 | CCCGTGGGACACAGGGGGGTCCACGAGAGAGTGATGCTCCAGCGCAAGGACAGAGCTTTCGGG | 206 | | |
| QY | 121 | CTCCGTGGGGGTCTGCTCTGGGACTGACAGAGATGAGAGGGACATGATGATGACAGAGAGGC | 180 | | |
| DB | 207 | CTCCGTGGGGGTCTGCTCTGGGACTGACAGAGATGAGAGGGACATGATGATGACAGAGAGGC | 266 | | |
| QY | 181 | AGTTCTGAGCCACAG | 240 | | |
| DB | 267 | AGTTCTGAGCCACAG | 326 | | |
| QY | 241 | TTCCGGGACAGAGATCCACAGAGTCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 300 | | |
| DB | 327 | TTCCGGGACAGAGATCCACAGAGTCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 386 | | |
| QY | 301 | ATGATACAGCTGCTGAGAGCCGACAGATGACATCCGCTTGGACGCCACAGTGAAGGACATCC | 360 | | |
| DB | 387 | ATGATACAGCTGCTGAGAGCCGACAGATGACATCCGCTTGGACGCCACAGTGAAGGACATCC | 446 | | |
| QY | 361 | CGGCGTCCCGGCGCTCCGCTACCTCTGATGATTTCTTACAGAGAGAGAGAGAGAGAGAGAG | 420 | | |
| DB | 447 | CGGCGTCCCGGCGCTCCGCTACCTCTGATGATTTCTTACAGAGAGAGAGAGAGAGAGAGAG | 506 | | |
| QY | 421 | CAGATGAGAGCGATCTCTCTGGGCGTGGATTTCCCTGACAGAGAGTCCCCAGCTGACAC | 480 | | |
| DB | 507 | CAGATGAGAGCGATCTCTCTGGGCGTGGATTTCCCTGACAGAGAGTCCCCAGCTGACAC | 566 | | |
| QY | 481 | CTGGGCGCTGCTGCTGCGCTCTGAGAGTACACCCAGAGTACTTAAAGATGAGAGAGAGAGAG | 540 | | |
| DB | 567 | CTGGGCGCTGCTGCTGCGCTCTGAGAGTACACCCAGAGTACTTAAAGATGAGAGAGAGAGAG | 626 | | |
| QY | 541 | TTGAGCGTGAAGTGTGGTGGGCAAGCGGATCTTCAAGGCCATCTCCATCCAGACATG | 600 | | |
| DB | 627 | TTGAGCGTGAAGTGTGGTGGGCAAGCGGATCTTCAAGGCCATCTCCATCCAGACATG | 686 | | |
| QY | 601 | TGGGCGACACTTCAGAGATTTTGCACCAAGCATGTGAGAGAGAGTCTAAGAGAGAGAGAGAG | 660 | | |
| DB | 687 | TGGGCGACACTTCAGAGATTTTGCACCAAGCATGTGAGAGAGAGTCTAAGAGAGAGAGAGAG | 746 | | |

[illegible]

| Accession | Sequence | Length |
|-----------|---|--------|
| Qy | 1741 GCAAGGACCAAAGGAGGCGACAGAGTGGACAGAGGGGGGCTCAGCTGGCTCGAATCCCGC | 1800 |
| Db | 1827 GCAAGGACCAAAGGAGGCGACAGAGTGGACAGAGGGGGCTCAGCTGGCTCGAATCCCGC | 1886 |
| Qy | 1801 CAGTCAGTGGTTACCTCTCCAGGGGAGTGCCTGGTGGCCAAACGGACCCAGGCTTTCAG | 1850 |
| Db | 1887 CAGTCAGTGGTTACCTCTCCAGGGGAGTGCCTGGTGGCCAAACGGACCCAGGCTTTCAG | 1946 |
| Qy | 1861 GAGCAGAGACGAGGGGCGAGGGGCGAGGGGACAGGAGAGGCCCTGCAATTTCTCTACGCCCAGG | 1920 |
| Db | 1947 GAGCAGAGACGAGGGGCGAGGGGCGAGGGGACAGGAGAGGCCCTGCAATTTCTCTACGCCCAGG | 2006 |
| Qy | 1921 TTCCGGAAGGTGTGAGACACAGGCCAGGTGCATGACAGTGGAGAGAGGGCGAGGCTTGA | 1980 |
| Db | 2007 TTCCGGAAGGTGTGAGACACAGGCCAGGTGCATGACAGTGGAGAGAGGGCGAGGCTTGA | 2066 |

RESULT 3
 ABQ73250 ID ABQ73250 standard; cDNA; 2852 BP.
 AC ABQ73250;
 XX 30-SEP-2002 (first entry)
 DT
 XX Human MAP kinase phosphatase splice form 2 cDNA sequence SEQ ID NO:2.
 DE
 XX Human; phosphatase; mitogen activated protein kinase phosphatase;
 KM MAP kinase; enzyme; chromosome 11; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Location/Qualifiers
 FH Key 1..56
 FT 5'UTR /*tag= a
 FT 57..2036
 FT CDS /*tag= D
 FT /product= "MAP kinase phosphatase splice form 2"
 FT 2037..2852
 FT /*tag= C
 FT
 TT
 XX
 XX WO200242436-A2.
 PN
 XX
 PD 30-MAY-2002.
 PD
 XX
 XX 07-NOV-2001; 2001WO-US42995.
 PF
 XX
 PR 20-NOV-2000; 2000US-0715177.
 PR 18-JAN-2001; 2001US-0761640.
 XX
 PA (PEKE) PE CORP NY.
 PA
 PI Wei M, Ketchum KA, Di Francesco V, Beasley EM;
 PI
 DR WPI: 2002-575237/61.
 DR P-PSDB; ABP51654.
 DR
 XX
 XX
 PT Novel isolated human phosphatase peptide useful for treating disorder
 PT characterized by absence of, inappropriate or unwanted expression of
 PT the phosphatase protein, and as immunogens to raise antibodies -
 PT
 XX
 PS Claim 1; Fig 1B; 85pp; English.
 PS
 CC The present invention describes an isolated human phosphatase peptide
 CC (I). (I) can be used for identifying a modulator of (I) by contacting
 CC (I) with an agent and determining if the agent has modulated the
 CC function or activity of (I). (I) is useful for identifying an agent that
 CC binds to (I), by contacting (I) with an agent and assaying the contacted
 CC mixture to determine whether a complex is formed with the agent bound
 CC (I). The human phosphatases from the present invention are mitogen
 CC activated protein (MAP) kinase phosphatases. These human MAP kinase
 CC phosphatases are located on chromosome 11. (I) and the polynucleotide
 CC sequences encoding (I) can be used in gene therapy. The present sequence

CC encodes human MAP kinase phosphatase splice form 2 from the present
 CC Invention.

XX Sequence 2852 BP; 674 A; 895 C; 807 G; 476 T; 0 other;

Query Match 99.9%; Score 1978.4; DB 24; Length 2852;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1979; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGACCTGGTCAAGTGAAGCGGTTGCCCCGGGAGCGGCGCTCCAGCGCCGTTGGG 60
 Db ATGACCTGGTCAAGTGAAGCGGTTGCCCCGGGAGCGGCGCTCCAGCGCCGTTGGG 116
 57 ATGACCTGGTCAAGTGAAGCGGTTGCCCCGGGAGCGGCGCTCCAGCGCCGTTGGG 116
 QY 61 CCTGGGACCAAGCGGTTCAAGGAGTCACTCCAGCGGAGCGAGGCTTTGGG 120
 Db CCTGGGACCAAGCGGTTCAAGGAGTCACTCCAGCGGAGCGAGGCTTTGGG 176
 117 CCTGGGACCAAGCGGTTCAAGGAGTCACTCCAGCGGAGCGAGGCTTTGGG 176
 QY 121 CTCCGTTGGGCTCTCTGGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 Db CTCCGTTGGGCTCTCTGGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
 177 CTCCGTTGGGCTCTCTGGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
 QY 181 AGTTCTGAGCCAAAGAGAGAGGCGCCAGTGAAGAGAGTCAAGCGGAGCGAGAGC 240
 Db AGTTCTGAGCCAAAGAGAGAGGCGCCAGTGAAGAGAGTCAAGCGGAGCGAGAGC 296
 237 AGTTCTGAGCCAAAGAGAGAGGCGCCAGTGAAGAGAGTCAAGCGGAGCGAGAGC 296
 QY 241 TTGGGGAAGATCCAGAGTCCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 300
 Db TTGGGGAAGATCCAGAGTCCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 356
 297 TTGGGGAAGATCCAGAGTCCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 356
 QY 301 ATGATCAGCTGTGAGGCGGAGATGATCCGCTGAGAGAGAGAGAGAGAGAGAGC 360
 Db ATGATCAGCTGTGAGGCGGAGATGATCCGCTGAGAGAGAGAGAGAGAGAGAGC 416
 357 ATGATCAGCTGTGAGGCGGAGATGATCCGCTGAGAGAGAGAGAGAGAGAGAGC 416
 QY 361 CGGCTCCCGGCTCCGCTAAGTGTGATGTTCTACAGAGAGAGAGAGAGAGAGC 420
 Db CGGCTCCCGGCTCCGCTAAGTGTGATGTTCTACAGAGAGAGAGAGAGAGAGC 476
 417 CGGCTCCCGGCTCCGCTAAGTGTGATGTTCTACAGAGAGAGAGAGAGAGAGC 476
 QY 421 CAGGATGAGAGCGGCTCTCTGGGAGTGAATTCCTGAGAGAGAGAGAGAGAGAGC 480
 Db CAGGATGAGAGCGGCTCTCTGGGAGTGAATTCCTGAGAGAGAGAGAGAGAGAGC 536
 477 CAGGATGAGAGCGGCTCTCTGGGAGTGAATTCCTGAGAGAGAGAGAGAGAGAGC 536
 QY 481 CTGGGCTGGTCTTGGCCCTCTGAGATGACACCCAGAGTGAATTAAGTGAAGAGAGC 540
 Db CTGGGCTGGTCTTGGCCCTCTGAGATGACACCCAGAGTGAATTAAGTGAAGAGAGC 596
 537 CTGGGCTGGTCTTGGCCCTCTGAGATGACACCCAGAGTGAATTAAGTGAAGAGAGC 596
 QY 541 TTGAGGCTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 600
 Db TTGAGGCTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 656
 597 TTGAGGCTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 656
 QY 601 TGGGACCACTCAGGATATTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGC 660
 Db TGGGACCACTCAGGATATTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGC 716
 657 TGGGACCACTCAGGATATTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGC 716
 QY 661 CCGGTTGGAGTGGCTCTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 720
 Db CCGGTTGGAGTGGCTCTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 776
 717 CCGGTTGGAGTGGCTCTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 776
 QY 721 AGCTGCTCAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 780
 Db AGCTGCTCAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 836
 777 AGCTGCTCAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 836
 QY 781 GAGCTGGCGGAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 840
 Db GAGCTGGCGGAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 896
 837 GAGCTGGCGGAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 896
 QY 841 AAGGTGTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 900
 Db AAGGTGTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 956
 897 AAGGTGTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 956
 QY 901 GAGCTGGCGTGGGCTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 960
 Db GAGCTGGCGTGGGCTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1016
 957 GAGCTGGCGTGGGCTCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1016

QY 961 CTGCTGTGGACACCGGAGACCGAGCTCCCGATCTTCCCACTTACTTGGGCTCA 1020
 Db CTGCTGTGGACACCGGAGACCGAGCTCCCGATCTTCCCACTTACTTGGGCTCA 1076
 1017 CTGCTGTGGACACCGGAGACCGAGCTCCCGATCTTCCCACTTACTTGGGCTCA 1076
 QY 1021 GAGTGAAGCGAGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1080
 Db GAGTGAAGCGAGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1136
 1077 GAGTGAAGCGAGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1136
 QY 1081 ATGACCGGAGAGATTGAACAATTCTGAGAGCTTCACTTCACTTCACTTCACTTCA 1140
 Db ATGACCGGAGAGATTGAACAATTCTGAGAGCTTCACTTCACTTCACTTCACTTCA 1196
 1137 ATGACCGGAGAGATTGAACAATTCTGAGAGCTTCACTTCACTTCACTTCACTTCA 1196
 QY 1141 TGGGATGAGAGTGGGCTCCAGCTGTCTCCGATGAGAGAGAGAGAGAGAGAGC 1200
 Db TGGGATGAGAGTGGGCTCCAGCTGTCTCCGATGAGAGAGAGAGAGAGAGAGC 1256
 1197 TGGGATGAGAGTGGGCTCCAGCTGTCTCCGATGAGAGAGAGAGAGAGAGAGC 1256
 QY 1201 GCTGCAAGAGACACAGGACCCAGCTGTCTGATGATGATGATGATGATGATGATG 1260
 Db GCTGCAAGAGACACAGGACCCAGCTGTCTGATGATGATGATGATGATGATGATG 1316
 1257 GCTGCAAGAGACACAGGACCCAGCTGTCTGATGATGATGATGATGATGATGATG 1316
 QY 1261 GCGGACACAGTGTGGCTTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1320
 Db GCGGACACAGTGTGGCTTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1376
 1317 GCGGACACAGTGTGGCTTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1376
 QY 1321 GCGGACAGTGAAGAGTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCG 1380
 Db GCGGACAGTGAAGAGTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCG 1436
 1377 GCGGACAGTGAAGAGTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCGAGCTCCG 1436
 QY 1381 CAGATCTACAGAGGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1440
 Db CAGATCTACAGAGGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1496
 1437 CAGATCTACAGAGGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1496
 QY 1441 GGTGGGCTTCCCGAGC 1500
 Db GGTGGGCTTCCCGAGC 1556
 1497 GGTGGGCTTCCCGAGC 1556
 QY 1501 CCGGACAGAGCTGAGGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1560
 Db CCGGACAGAGCTGAGGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1616
 1557 CCGGACAGAGCTGAGGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1616
 QY 1561 GCCCGGAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1620
 Db GCCCGGAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1676
 1617 GCCCGGAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1676
 QY 1621 ATCAGTCTTGTGAGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1680
 Db ATCAGTCTTGTGAGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1736
 1677 ATCAGTCTTGTGAGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1736
 QY 1681 GAGGTCTTCTTCCAGAGAGTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1740
 Db GAGGTCTTCTTCCAGAGAGTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1796
 1737 GAGGTCTTCTTCCAGAGAGTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1796
 QY 1741 GCAAGGACCAAGC 1800
 Db GCAAGGACCAAGC 1856
 1797 GCAAGGACCAAGC 1856
 QY 1801 CAGTCAAGTGTATTAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1860
 Db CAGTCAAGTGTATTAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1916
 1857 CAGTCAAGTGTATTAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1916
 QY 1861 GAGGAGC 1920
 Db GAGGAGC 1976
 1917 GAGGAGC 1976
 QY 1921 TTCCGAGC 1980
 Db TTCCGAGC 2036
 1977 TTCCGAGC 2036

RESULT 4
 AAD36063
 ID AAD36063 standard; cDNA; 2618 BP.
 XX

| | |
|----------------------------|---|
| AC | AAD36063; |
| XX | |
| DT | 09-AUG-2002 (first entry) |
| DE | Murine dual-specificity phosphatase 15 (DSP-15) cDNA. |
| XX | |
| KW | Murine; dual-specificity phosphatase 15; DSP15; anti-allergic; cytostatic; immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme; signal transduction; cell proliferation; Duchenne muscular dystrophy; cell cycle abnormality; graft-versus-host disease; autoimmune disease; metabolic disease; allergy; screening; gene; se. |
| KM | |
| XX | |
| OS | Mus musculus. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | CDS 35..1450 |
| FT | /tag= a |
| FT | /product= "Murine DSP-15 protein" |
| FN | WO200224740-A2. |
| PD | |
| XX | |
| PE | 19-SEP-2001; 2001WC-US29406. |
| PR | 19-SEP-2000; 2000US-233833P. |
| PR | 18-SEP-2001; 2001US-0955732. |
| PA | (CEPT-) CEPTVR INC. |
| PI | Luche RM, Wei B; |
| DR | WPI; 2002-394127/42. |
| XX | |
| DR | P-P5DB; AAE22735. |
| XX | |
| PT | New dual-specificity phosphatase 15 polypeptide and polynucleotides, useful for treating e.g. Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases - |
| PS | Claim 56; Fig 4; 91pp; English. |
| CC | The invention relates to a new isolated dual-specificity phosphatase 15 (DSP-15) polypeptide which retains the ability to dephosphorylate an activated MAP (mitogen activated protein) kinase. DSPs are phosphatases that dephosphorylate both phosphotyrosine and phosphothreonine/serine residues. DSP-15 polypeptides may be used to identify agents that modulate DSP-15 activity, where such agents may inhibit or enhance signal transduction via a MAP-kinase cascade, leading to cell proliferation. DSP polypeptides may be used to modulate DSP-15 activity in a patient, and to ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft- versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. DSP-15 alternate form polypeptides are useful in screening assays for modulators of enzyme activity and/or substrate binding. The present sequence is murine DSP-15 cDNA. |
| SQ | Sequence 2618 BF; 538 A; 857 C; 763 G; 454 T; 0 other: |
| Query Match | 89.6%; Score 1774; DB 24; Length 2618; |
| Best Local Similarity | 95.1%; Pred. No. 0; |
| Matches 1882; Conservative | 0; Mismatches 0; Indels 98; Gaps 1 |
| DG | |
| 1 | ATGGCCTCGTGCACGTGAAGCGTTGCCCGGGGACAGGGCGCTCCAGCCCGTGAGG 60 |
| 35 | ATGGCCTCGTGCACGTGAAGCGTTGCCCGGGGACAGGGCGCTCCAGCCCGTGAGG 94 |
| 61 | CCCTGGGACCAGCGCGGTTCAGGCAAGAATCATCTCACGCAAGACAGACTTGGCGGTG 120 |
| 95 | CCCTGGGACCAGCGCGGTTCAGGCAAGAATCATCTCACGCAAGACAGACTTGGCGGTG 154 |
| 121 | CTCCGTGGGCGCTCTCTCGGCACTCCAGAGATGAGAGGAGCAATTATGATGACGACAGAGCC 180 |

| | | | |
|----|------|--|------|
| Db | 155 | CTCCGTGGGGGTGTCTCCCTGGAGACTTCGACAGATTGGAAGGGGACATGATGTATGACGACGAGGCC | 214 |
| Oy | 181 | AGTCTAGGCCCAACAGAGAAAGGCCCCCGAGTAGGAGAGAGCTCCAGCGGAGCCACAGACAGAC | 240 |
| Db | 215 | AGTTCTAGCCCAACAGAGAAAGGCCCCCGAGTAGGAGAGAGCTCCAGCGGAGCCACAGACAGAC | 274 |
| Oy | 241 | TTCCGGGCAAGGATCCACAGAGTCCCCAGAAAGCAGAGAGACAGAGGACAGACCTTCACCTTC | 300 |
| Db | 275 | TTCCGGGCAAGGATCCACAGAGTCCCCAGAAAGCAGAGAGAGAGAGGACAGACCTTCACCTTC | 334 |
| Oy | 301 | ATGGTACAGCTGCCTGAGAGGCCGACAGATGACATCCGCTGGAGAGCCACGCTGAGAGCACCC | 360 |
| Db | 335 | ATGGTACAGCTGCCTGAGAGGCCGACAGATGACATCCGCTGGAGAGCCACGCTGAGAGCACCC | 394 |
| Oy | 361 | CGGCTCCCGGCTCCGCTACCTGTCTGGTAGTTTCTACACGAGAGAGAAAGGTTCTGAGC | 420 |
| Db | 395 | CGGCTCCCGGCTCCGCTACCTGTCTGGTAGTTTCTACACGAGAGAGAAAGGTTCTGAGC | 454 |
| Oy | 421 | CAGGATGAGACGGTTCCTCCCTGGGGGTGGATTTCCTCCCTACACGACGCTCCCGAGTGCAC | 480 |
| Db | 455 | CAGGATGAGACGGTTCCTCCCTGGGGGTGGATTTCCTCCCTACACGACGCTCCCGAGTGCAC | 514 |
| Oy | 481 | CTGGGCTGTGCTTTGCCCTCTGGAGTGACACCAGGTGTACTTAGTAGAGACGGGGGC | 540 |
| Db | 515 | CTGGGCTGTGCTTTGCCCTCTGGAGTGACACCAGGTGTACTTAGTAGAGACGGGGGC | 574 |
| Oy | 541 | TTACGCTGACGTGTGGTGGCAAAAGCCGATCTTCAAGGCCATCTCCATCCACATG | 600 |
| Db | 575 | TTACGCTGTACGTGTGGTGGCAAAAGCCGATCTTCAAGGCCATCTCCATCCACATG | 634 |
| Oy | 601 | TGGGCAACACTCCAGAGTATGACCAAGCAATGTATGAGACACTCTAGGACACGGGCTTGTA | 660 |
| Db | 635 | TGGGCAACACTCCAGAGTATGACCAAGCAATGTATGAGACACTCTAGGACACGGGCTTGTA | 694 |
| Oy | 661 | CCGGGTGGCAGTGCCTCTACCTGGGCCAGCCACTACACGAGAGACTGAACTCCGAACAG | 720 |
| Db | 695 | CCGGGTGGCAGTGCCTCTACCTGGGCCAGCCACTACACGAGAGACTGAACTCCGAACAG | 754 |
| Oy | 721 | AGCTGCCTCAATAGTGTGACGGGCTATGGCCGACCTGGAGTCTGCGGGGCTCCACGAGGC | 780 |
| Db | 755 | AGCTGCCTCAATAGTGTGACGGGCTATGGCCGACCTGGAGTCTGCGGGGCTCCACGAGGC | 814 |
| Oy | 781 | GAGCCTTGGCGGGTCTCAGAAACAGAACAGATGAGACAGGCGATCCGTGTAGACTGTGG | 840 |
| Db | 815 | GAGCCTTGGCGGGTCTCAGAAACAGAACAGATGAGACAGGCGATCCGTGTAGACTGTGG | 874 |
| Oy | 841 | AAAGTGTGATGTCACTGATGACCTTGAAGATGTCACTTCCAAAGAGATCCCGCAGGCTGTG | 900 |
| Db | 875 | AAAGTGTGATGTCACTGATGACCTTGAAGATGTCACTTCCAAAGAGATCCCGCAGGCTGTG | 934 |
| Oy | 901 | GAGGTGGGCCCTGGGGGCTCCGCTCCAGCAGATCCGTACTTCATGCAACAACAGATGCTG | 960 |
| Db | 935 | GAGGTGGGCCCTGGGGGCTCCGCTCCAGCAGATCCGTACTTCATGCAACAACAGATGCTG | 994 |
| Oy | 961 | CTGCTGTGTGCACAGCGGAGCCAGGCTCCGCACTTTCCGCCACTCTTACCTTGGGCTCA | 1020 |
| Db | 995 | CTGCTGTGTGCACAGCGGAGCCAGGCTCCGCACTTTCCGCCACTCTTACCTTGGGCTCA | 1054 |
| Oy | 1021 | GAGGTGAAACGAGCAAACTGTGAGAGACTGTGAGAGAAACAGGGTCACTCCACTTTGTAAC | 1080 |
| Db | 1055 | GAGGTGAAACGAGCAAACTGTGAGAGACTGTGAGAGAAACAGGGTCACTCCACTTTGTAAC | 1114 |
| Oy | 1081 | ATGACCCCGGAGATTGACAACTTCTACCTTGAGGCTTCACTTACACAAATGTGGGCTCTC | 1140 |
| Db | 1115 | ATGACCCCGGAGATTGACAACTTCTACCTTGAGGCTTCACTTACACAAATGTGGGCTCTC | 1174 |
| Oy | 1141 | TGGGATGAGAGATGTGGCCCAAGCTCTGCCGCACTTGAAGAGAGACGCAACCGTTATTTAG | 1200 |
| Db | 1175 | TGGGATGAGAGATGTGGCCCAAGCTCTGCCGCACTTGAAGAGAGACGCAACCGTTATTTAG | 1234 |
| Oy | 1201 | GCTCAAGAGACAGGGGCAACCAAGCTGTGCTCACTGCAAGATGGGCTGTAGCGGCTCA | 1260 |

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Db      1235 GCTGCAGAGACACAGGGGACCCACGTCGTGCTCCACTGCAAGATGGGCTCCTCA 1294
QY      1261 GGCGCCACAGTGTGCTGCTTATGCGATGAAGCAGTACGATGAGCCTGAGAGGCGCTG 1320
Db      1295 GGCGCCACAGTGTGCTGCTTATGCGATGAAGCAGTACGATGAGCCTGAGAGGCGCTG 1354
QY      1321 CGCGCAGTGAAGAGTCCGCGCCATGCGCCCGCCCAACCTTGCGCTTCTGCGCACTG 1380
Db      1355 CGCGCAGTGAAGAGTCCGCGCCATGCGCCCGCCCAACCTTGCGCTTCTGCGCACTG 1414
QY      1381 CAGATCTACAGGGGACATCTGACGCGGACCGCCAGAGCCGATGCTGGAGAGAAAGTG 1440
Db      1415 CAGATCTACAGGGGACATCTGACG----- 1438
QY      1441 GGTGGGCTCTCCCGACAGAGACCCAGGCCCTGAACTCTACACATTTCCACCTCTT 1500
Db      1439 ----- 1438
QY      1501 CGCGCAGAACCTGAGGGGTGTGGGAGGAAAGTTGTAGCATGGAAGAGCCAGAGCA 1560
Db      1439 --GCCGAACTGAGGGGTGTGGGAGGAAAGTTGTAGCATGGAAGAGCCAGAGCA 1496
QY      1561 GCCCGGAAAGAGAGCTGGGCGACGCGCCACGATTAACCTCCGAGGGGTCTATGAGTCC 1620
Db      1497 GCCCGGAAAGAGAGCTGGGCGACGCGCCACGATTAACCTCCGAGGGGTCTATGAGTCC 1556
QY      1621 ATAGTCTTCTGAGAGCTTCTGAGCTGAGAGACCTCAAGACAGTACATGCAATGCCA 1680
Db      1557 ATAGTCTTCTGAGAGCTTCTGAGCTGAGAGACCTCAAGACAGTACATGCAATGCCA 1616
QY      1681 GAGGTCTTCTGAGAGCTTCTGAGCTGAGAGACCTCAAGACAGTACATGCAATGCCA 1740
Db      1617 GAGGTCTTCTGAGAGCTTCTGAGCTGAGAGACCTCAAGACAGTACATGCAATGCCA 1676
QY      1741 GCAAGAGCCAGAGAGAGCCAGAGAGTGAACAGGGGGCTCAAGCTCCGTAAGTCCGC 1800
Db      1677 GCAAGAGCCAGAGAGAGCCAGAGAGTGAACAGGGGGCTCAAGCTCCGTAAGTCCGC 1736
QY      1801 CAGTCACTGTTACCTCCAGAGGAGTGCCTGCTGCTGAGCCACCGACCTTCCAG 1860
Db      1737 CAGTCACTGTTACCTCCAGAGGAGTGCCTGCTGCTGAGCCACCGACCTTCCAG 1796
QY      1861 GAGCAGAGACAGAGGAGAGGGGAGAGGAGAGAGCCCTGATTTCTTACGCCACAG 1920
Db      1797 GAGCAGAGACAGAGGAGAGGGGAGAGGAGAGAGCCCTGATTTCTTACGCCACAG 1856
QY      1921 TTCGGAGAGTGTGAGACAGCCAGCTGATGACAGTGAAGAGAGGGGCGAGGCTTGA 1980
Db      1857 TTCGGAGAGTGTGAGACAGCCAGCTGATGACAGTGAAGAGAGGGGCGAGGCTTGA 1916

RESULT 5
AB073249
ID      AB073249 standard; cDNA; 2704 BP.
XX
XX      AB073249;
XX
XX      30-SEP-2002 (first entry)
XX
DE      Human MAP kinase phosphatase splice form 1 cDNA sequence SEQ ID NO.1.
XX
XX      Human; phosphatase; mitogen activated protein kinase phosphatase;
XX      MAP kinase; enzyme; chromosome 11; gene; ss.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      FT      1..93
XX      FT      5'UTR      /*tag= a
XX      FT      CDS      94..1509
XX      FT      /*tag= b
XX      FT      /product= "MAP kinase phosphatase splice form 1"
XX      FT      1510..2704
XX      FT      3'UTR

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FT      /*tag= c
XX      MO200242436-A2.
XX
XX      30-MAY-2002.
XX
XX      07-NOV-2001; 2001WO-US42995.
XX
XX      20-NOV-2000; 2000US-0715177.
XX      18-JAN-2001; 2001US-0761640.
XX
XX      (PERE ) PE CORP NY.
XX
XX      Wei M, Ketchum KA, Di Francesco V, Beasley EM;
XX      P-PDB; ABP51653.
XX
XX      MPI; 2002-575237/61.
XX
XX      Novel isolated human phosphatase peptide useful for treating disorder
XX      characterized by absence of, inappropriate or unwanted expression of
XX      the phosphatase protein, and as immunogens to raise antibodies
XX
XX      Claim 1; Fig 1A; 85pp; English.
XX
XX      The present invention describes an isolated human phosphatase peptide
XX      (I). (I) can be used for identifying a modulator of (I) by contacting
XX      (I) with an agent and determining if the agent has modulated the
XX      function or activity of (I). (I) is useful for identifying an agent that
XX      binds to (I), by contacting (I) with an agent and assaying the contacted
XX      mixture to determine whether a complex is formed with the agent bound
XX      (I). The human phosphatases from the present invention are mitogen
XX      activated protein (MAP) kinase phosphatases. These human MAP kinase
XX      phosphatases are located on chromosome 11. (I) and the polynucleotide
XX      sequences encoding (I) can be used in gene therapy. The present sequence
XX      encodes human MAP kinase phosphatase splice form 1 from the present
XX      invention.
XX
XX      Sequence 2704 BP; 569 A; 874 C; 794 G; 467 T; 0 other;
XX
XX      Query Match      89.6%; Score 1774; DB 24; Length 2704;
XX      Best Local Similarity 95.1%; Pred. No. 0;
XX      Matches 1882; Conservative 0; Mismatches 0; Indels 98; Gaps 1;
XX
QY      1 ATGGCCCTGTCACAGTGAAGCCGCTGCGCCGCGGACGCGGCGCTCCAGCCCGTGGG 60
Db      94 ATGGCCCTGTCACAGTGAAGCCGCTGCGCCGCGGACGCGGCGCTCCAGCCCGTGGG 153
QY      61 CCTGGGACAGGGGGGTCCAGCGAAGAGTCACTCCAGCGAAAGCAGAGCTTGGCGTG 120
Db      154 CCTGGGACAGGGGGGTCCAGCGAAGAGTCACTCCAGCGAAAGCAGAGCTTGGCGTG 213
QY      121 CTCCTGGGGGTGTCTCTGCGGATGCGAGATGAGAGGGGACATATGATGACGAGGCC 180
Db      214 CTCCTGGGGGTGTCTCTGCGGATGCGAGATGAGAGGGGACATATGATGAGAGGCC 273
QY      214 AGTCTGAGCCACAGAGAGAGCCCGCAGTGAAGAGAGCTCCACCGGGGACAGACAGAC 240
Db      274 AGTCTGAGCCACAGAGAGAGCCCGCAGTGAAGAGAGCTCCACCGGGGACAGACAGAC 333
QY      241 TTCGGGCAAGATGCCAGAGTCCCGAGAGCAGAGAGAGAGAGGACGACCTGCACTTC 300
Db      334 TTCGGGCAAGATGCCAGAGTCCCGAGAGCAGAGAGAGAGAGAGGACGACCTGCACTTC 393
QY      301 ATGGTACAGCTGCTGAGAGCGCGAGATGACATCGCTGCGACCGCAGCTGAGAGCACCC 360
Db      394 ATGGTACAGCTGCTGAGAGCGCGAGATGACATCGCTGCGACCGCAGCTGAGAGCACCC 453
QY      361 CGGCTTCCCGGCTCCGCTACCTGCTGTGATGTTTTCACAGAGAGAGAGAGGCTTGAAG 420
Db      454 CGGCTTCCCGGCTCCGCTACCTGCTGTGATGTTTTCACAGAGAGAGAGAGGCTTGAAG 513
QY      421 CAGGATGAGAGGATCTCTGCGGGGTGATTTCCCTGACAGAGAGCTCCCGACCTGACAC 480

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| | | | |
|----|------|---|------|
| Db | 514 | CAGAGTAGAGAGGCTCTCTCTG36GGGTGGATTTTCCCTGTACAGACAGCTCCGCCAGCTGCACCC | 573 |
| Qy | 481 | CTG3G3CCTGATCTTGGCCCTCTTGGAGTGACACCCAGATGTACTTAAATGAGAGAGGGGGCC | 540 |
| Db | 574 | CTGG3GCCCTGGATCTTGGCCCTCTTGGAGTGACACCCAGGATGTACTTAAATGAGAGAGGGGGCC | 633 |
| Qy | 541 | TTTCAAGCGTAGATCTGGTGGGCGAAGCCGAGATCTTCAAGCGCCATCTCATCCAGACATG | 600 |
| Db | 634 | TTTCAAGCGTAGATCTGGTGGGCGAAGCCGAGATCTTCAAGCGCCATCTCATCCAGACATG | 693 |
| Qy | 601 | TGGGCGACACTCCACAGTATTGCACTCCACCAAGCATGTAGAGGCAAGCTCTAAGCGACGCGCTTTGTA | 660 |
| Db | 694 | TGGGCGACACTCCACAGTATTGCACTCCACCAAGCATGTAGAGGCAAGCTCTAAGCGACGCGCTTTGTA | 753 |
| Qy | 661 | CCGGGTGGCAATGGCCCTTCACTGGGGCGACGCACTACCAAGAGAGACTGAATCTCGGAACAG | 720 |
| Db | 754 | CCGGGTGGCAATGGCCCTTCACTGGGGCGACGCACTACCAAGAGAGACTGAATCTCGGAACAG | 813 |
| Qy | 721 | AGCTGGCTCAATGAGATGAGATGAGACGAGCTATGAGCCAGACTGAGATCTCTGGGGCTTCCACGCGCC | 780 |
| Db | 814 | AGCTGGCTCAATGAGATGAGATGAGACGAGCTATGAGCCAGACTGAGATCTCTGGGGCTTCCACGCGCC | 873 |
| Qy | 781 | GAGCTTGGCGGGGTCTCTCAAGACAGAGAGAGATGAGACAGGAGGATCCGTGCTGAGCTGTGG | 840 |
| Db | 874 | GAGCTTGGCGGGGTCTCTCAAGACAGAGAGAGATGAGACAGGAGGATCCGTGCTGAGCTGTGG | 933 |
| Qy | 841 | AAAGTGTTGATAGTACAGTACGACTTGAGAGTGTCACTTCCAAAGAGATCCGCGAGGCTTG | 900 |
| Db | 934 | AAAGTGTTGATAGTACAGTACGACTTGAGAGTGTCACTTCCAAAGAGATCCGCGAGGCTTG | 993 |
| Qy | 901 | GAGCTGCGGCTTGGGGCTCTCCCTCTCAGACAGTACCGTGACTTCACTGACAAACAAGATCGTG | 960 |
| Db | 994 | GAGCTGCGGCTTGGGGCTCTCCCTCTCAGACAGTACCGTGACTTCACTGACAAACAAGATCGTG | 1053 |
| Qy | 961 | CTGCTGATGTGGACACAGCGGAGCCGAGCCCTCCGCAATCTTCCGCCACTTACCTTGAGGCTCA | 1020 |
| Db | 1054 | CTGCTGATGTGGACACAGCGGAGCCGAGCCCTCCGCAATCTTCCGCCACTTACCTTGAGGCTCA | 1113 |
| Qy | 1021 | GAGTGGAAACGACAGCAAACTTGAGAGGCTGACAGAGAAACAGGGTACCCACATCTTGAAC | 1080 |
| Db | 1114 | GAGTGGAAACGACAGCAAACTTGAGAGGCTGACAGAGAAACAGGGTACCCACATCTTGAAC | 1173 |
| Qy | 1081 | ATGGCCCGGGAGATTGACAATCTTACACTGAGCGCTTCACTACCAACATGTGGGCTC | 1140 |
| Db | 1174 | ATGGCCCGGGAGATTGACAATCTTACACTGAGCGCTTCACTACCAACATGTGGGCTC | 1233 |
| Qy | 1141 | TGGGATGAGAGTGGGCCCAAGCTGTGCGGACCTGGAAGAGAGACGCAACCGCTTCAATTGAG | 1200 |
| Db | 1234 | TGGGATGAGAGTGGGCCCAAGCTGTGCGGACCTGGAAGAGAGACGCAACCGCTTCAATTGAG | 1293 |
| Qy | 1201 | GCTGCAAGAGACACAGGGGACCCACAGTGGTGTCCACTGCAAGATGGGGGTCAAGCGGCTCA | 1260 |
| Db | 1294 | GCTGCAAGAGACACAGGGGACCCACAGTGGTGTCCACTGCAAGATGGGGGTCAAGCGGCTCA | 1353 |
| Qy | 1261 | GCGGCGACAGTGTGGGCTTATGCACTGAAGAGAGTACGATCAGCTGAGACAGGCGCTG | 1320 |
| Db | 1354 | GCGGCGACAGTGTGGGCTTATGCACTGAAGAGAGTACGATCAGCTGAGACAGGCGCTG | 1413 |
| Qy | 1321 | CGCCACGTGACAGAGAGCTCCGGGCGCATGCGCGGCGCCCAACCTGTGTTTCTTGCGCCAGTGT | 1380 |
| Db | 1414 | CGCCACGTGACAGAGAGCTCCGGGCGCATGCGCGGCGCCCAACCTGTGTTTCTTGCGCCAGTGT | 1473 |
| Qy | 1381 | CAGATCTTACACAGGGGATCTCTGACGCGCACGCGCAGAACCATGTTGGAGACAGAAAGTG | 1440 |
| Db | 1474 | CAGATCTTACACAGGGGATCTCTGACG----- | 1497 |
| Qy | 1441 | GGTGGGGTCTCCCGACAGAGAGACCCAGGCCCTGTAAGTCTTACACCATTCCTCCACTCTT | 1500 |
| Db | 1498 | ----- | 1497 |
| Qy | 1501 | CCGCCAGAACCTGAAGGATGTGGGGAGAGAAAGTGTAAAGCATGAAGAGACCGACGCA | 1566 |
| Db | 1498 | --GCCAGAACCTGAAGGATGTGGGGAGAGAAAGTGTAAAGCATGAAGAGACCGACGCA | 1555 |

PA (PEXE) PE CORP NY.
XX
PI Wei M, Ketchum KA, Di Francesco V, Beasley EM,
XX
DR MPI, 2002-575237/61.
DR F-PSDB; ABP51653.
XX
XX Novel isolated human phosphatase peptide useful for treating disorder
PT characterized by absence of, inappropriate or unwanted expression of
PT the phosphatase protein, and as immunogens to raise antibodies -
XX
XX Claim 1, Fig 3a, 85pp; English.
XX
XX The present invention describes an isolated human phosphatase peptide
CC (I). (I) can be used for identifying a modulator of (I) by contacting
CC (I) with an agent and determining if the agent has modulated the
CC function or activity of (I). (I) is useful for identifying an agent that
CC binds to (I), by contacting (I) with an agent and assaying the contacted
CC mixture to determine whether a complex is formed with the agent bound
CC (I). The human phosphatases from the present invention are mitogen
CC activated protein (MAP) kinase phosphatases. These human MAP kinase
CC phosphatases are located on chromosome 11. (I) and the polynucleotide
CC sequences encoding (I) can be used in gene therapy. The present sequence
CC encodes human MAP kinase phosphatase splice form 1 from the present
CC invention.
XX
XX Sequence 2704 BP; 569 A; 874 C; 794 G; 467 T; 0 other;
SQ
Query Match 89.6%; Score 1774; DB 24; Length 2704;
Best Local Similarity 95.1%; Pred No. 0;
Matches 1882; Conservative 0; Mismatches 0; Indels 98; Gaps 1;
QY 1 ATGGCCCTTGTGCAAGTGAAGCCGTTGCCCCGAGGAGGCGCCCTCCAGCCCTGGAG 60
DB 94 ATGGCCCTTGTGCAAGTGAAGCCGTTGCCCCGAGGAGGCGCCCTCCAGCCCTGGAG 153
QY 61 CCTGGGACACAGGCGGTCCAGGAGAGAGTGCATCCAGCCGAGAGAGAGAGAGAGAGAG 120
DB 154 CCTGGGACACAGGCGGTCCAGGAGAGAGTGCATCCAGCCGAGAGAGAGAGAGAGAGAG 213
QY 121 CTCGCTGGGCTGTCTCTGGAGTGCAGAGTGAAGGAGGAGCAATGATGATGACAGAGAG 180
DB 214 CTCGCTGGGCTGTCTCTGGAGTGCAGAGTGAAGGAGGAGCAATGATGATGACAGAGAG 273
QY 181 AGTTCTGAGCCCAAG 240
DB 274 AGTTCTGAGCCCAAG 333
QY 241 TTCGGGCAAGAGATCCAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 334 TTCGGGCAAGAGATCCAGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 393
QY 301 ATGTGACAGCTGTGAGGCGGAGAGATGATCCGCTGGAGAGAGAGAGAGAGAGAGAGAG 360
DB 394 ATGTGACAGCTGTGAGGCGGAGAGATGATCCGCTGGAGAGAGAGAGAGAGAGAGAGAG 453
QY 361 CGGCTCCCGGCTCCGCTACTGCTGAGTGTGATGATGATGATGATGATGATGATGATGAT 420
DB 454 CGGCTCCCGGCTCCGCTACTGCTGAGTGTGATGATGATGATGATGATGATGATGATGAT 513
QY 421 CAGGATGAGAGAGTCTCTCTGGAGCGTGAATTTCCCTGACAGAGAGTCCCGAGCTGACAC 480
DB 514 CAGGATGAGAGAGTCTCTCTGGAGCGTGAATTTCCCTGACAGAGAGTCCCGAGCTGACAC 573
QY 481 CTGGGCGCTGTGTTGGCCCTCTGGAGTGAACCCAGGTGTACTTGAATGAGAGAGAGAGAG 540
DB 574 CTGGGCGCTGTGTTGGCCCTCTGGAGTGAACCCAGGTGTACTTGAATGAGAGAGAGAGAG 633
QY 541 TTCAAGCTGACGCTGTGAGGAG 600
DB 634 TTCAAGCTGACGCTGTGAGGAG 693
QY 601 TGGGCAACACTCCAGGTATTGACCAAGAGATGTAGGAGAGCTCTTAGGAGAGGCGCTTGTGA 660

DB 694 TGGGCAACACTCCAGGTATTGACCAAGAGATGTAGGAGAGCTTAGGAGAGGCGCTTGTGA 753
QY 661 CCGGATGAGAGTGTCT 720
DB 754 CCGGATGAGAGTGTCT 813
QY 721 AGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 814 AGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 873
QY 781 GAGCTGCGCGGTCTCTCAAG 840
DB 874 GAGCTGCGCGGTCTCTCAAG 933
QY 841 AAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 934 AAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
QY 901 GAGCTGCGCGGTCTCTCAAG 960
DB 994 GAGCTGCGCGGTCTCTCAAG 1053
QY 961 CTGCTGTGAGACAGCGGAG 1020
DB 1054 CTGCTGTGAGACAGCGGAG 1113
QY 1021 GAGTGAAG 1080
DB 1114 GAGTGAAG 1173
QY 1081 ATGGCCCGGAGATGACAACTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1174 ATGGCCCGGAGATGACAACTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
QY 1141 TGGGATGAGAGTGTGAG 1200
DB 1234 TGGGATGAGAGTGTGAG 1293
QY 1201 GCTGCAAG 1260
DB 1294 GCTGCAAG 1353
QY 1261 GCGGACCAAGTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1320
DB 1354 GCGGACCAAGTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1413
QY 1321 CGCCAGTGAAGAGAGTCCGAGCCATGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1414 CGCCAGTGAAGAGAGTCCGAGCCATGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1473
QY 1381 CAGATCTACAGAGAGAGTCTGAGCGCCAGCGCCAGAGCCATGTCTGGAGAGAGAGAGAG 1440
DB 1474 CAGATCTACAGAGAGAGTCTGAGCGCCAGCGCCAGAGCCATGTCTGGAGAGAGAGAGAG 1497
QY 1441 GGTGGGCTCTCCCAAG 1500
DB 1498 ----- 1497
QY 1501 CCGCAG 1560
DB 1498 --GCGAG 1555
QY 1561 GCGCCGAG 1620
DB 1556 GCGCCGAG 1615
QY 1621 ATCAGTCTTGTGAG 1680
DB 1616 ATCAGTCTTGTGAG 1675
QY 1681 GAGTCTTCTCTTCCAG 1740

```

RESULT 7
ABL40805
ID ABL40805 standard; cDNA; 2322 BP.
xx

```

Human MAP kinase phosphatase-1-like enzyme encoding cDNA

W0200220732-A2

PS Claim 1; Fig 13; 134pp; English.

SQ Sequence 2322 BP; 467 A; 751 C; 718 G; 386 T; 0 other;

SQ Sequence 2322 BP; 467 A; 751 C; 718 G; 386 T; 0 other;

| | Homo sapiens. | Location/Qualifiers |
|-----------------|-------------------------------|---|
| US | | |
| XX | | |
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| FT | CDS | /tag= a |
| FT | | /product= "MAP kinase phosphatase-like enzyme" |
| FT | | /note= "contains internal codon deletions" |
| FT | | /transl_except= "(pos: 156..157, aa: Leu)" |
| FT | | /note= "there is an apparent one codon deletion which alters the reading frame" |
| FT | | /transl_except= "(pos: 180..181, aa: Arg)" |
| FT | | /note= "there is an apparent one codon deletion which alters the reading frame" |
| FT | | /transl_except= "(pos: 414..415, aa: Val)" |
| FT | | /note= "there is an apparent one codon deletion which alters the reading frame" |
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| FT | | /note= "there is an apparent one codon deletion which alters the reading frame" |
| FT | | /transl_except= "(pos: 2088..2089, aa: Xaa)" |
| FT | | /note= "there is an apparent one codon deletion which alters the reading frame" |
| WO200220732-A2. | | |
| XX | | |
| PD | 14-MAR-2002. | |
| XX | | |
| PF | 27-AUG-2001; 2001WO-EP09848. | |
| XX | | |
| PR | 07-SEP-2000; 2000OUS-230709P. | |
| XX | | |
| PA | (FARB.) BAYER AG. | |
| XX | | |
| PI | Llou J; | |
| XX | | |
| WPI: | 2002-339802/37. | |
| DR | P-PDB; ABB07845. | |
| XX | | |

CC mixture to determine whether a complex is formed with the agent bound
CC (1). The human phosphatases from the present invention are mitogen
CC activated protein (MAP) kinase phosphatases. These human MAP kinase
CC phosphatases are located on chromosome 11. (1) and the polynucleotide
CC sequences encoding (1) can be used in gene therapy. The present sequence
CC encodes human MAP kinase phosphatase splice form 3 from the present
CC invention.

XX Sequence 2540 BP; 552 A; 809 C; 739 G; 440 T; 0 other;

Query Match 68.0%; Score 1345.6; DB 24; Length 2540;
Best Local Similarity 85.1%; Pred. No. 3e-275; Indels 291; Gaps 5;
Matches 1689; Conservative 0; Mismatches 4;

```
QY 1 ATGGCCCTGGTCACTGAGCCGCTTGGCCCGGAGCGGCGCTTCCAGCGCCGCGG 60
DB ATGGCCCTGGTCACTGAGCCGCTTGGCCCGGAGCGGCGCTTCCAGCGCCGCGG 147
QY 61 CCCTGGGACCCAGCGCGCTCCAGCGAGAGTCCGACTCCAGCGAGAGGCGACTTTGCGGTG 120
DB CCCTGGGACCCAGCGCGCTCCAGCGAGAGTCCGACTCCAGCGAGAGGCGACTTTGCGGTG 207
QY 121 CTCCTGGGGGCTCTCTGGGAGCTGCGAGATGAGGGGAGCAATGATGATGACAGAGGCGC 180
DB CTCCTGGGGGCTCTCTGGGAGCTGCGAGATGAGGGGAGCAATGATGATGACAGAGGCGC 267
QY 208 CTCCTGGGGGCTCTCTGGGAGCTGCGAGATGAGGGGAGCAATGATGATGACAGAGGCGC 267
DB CTCCTGGGGGCTCTCTGGGAGCTGCGAGATGAGGGGAGCAATGATGATGACAGAGGCGC 327
QY 181 AGTTCTGAGCCACAGAGAGGCGCCGAGTGAAGAGAGCTCCAGCGGAGCCAGAC 240
DB AGTTCTGAGCCACAGAGAGGCGCCGAGTGAAGAGAGCTCCAGCGGAGCCAGAC 327
QY 241 TTGGGGAGAGATCCCAAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB TTGGGGAGAGATCCCAAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
QY 328 TTGGGGAGAGATCCCAAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
DB TTGGGGAGAGATCCCAAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 301 ATGTGACAGTGTGAGGCGCGAGAGATGACATCGGCTGGAGAGAGAGAGAGAGAGAGAGAG 360
DB ATGTGACAGTGTGAGGCGCGAGAGATGACATCGGCTGGAGAGAGAGAGAGAGAGAGAGAG 447
QY 388 ATGTGACAGTGTGAGGCGCGAGAGATGACATCGGCTGGAGAGAGAGAGAGAGAGAGAGAG 447
DB ATGTGACAGTGTGAGGCGCGAGAGATGACATCGGCTGGAGAGAGAGAGAGAGAGAGAGAG 507
QY 448 CGGCTTCCCGGCTCCGCTACCTGCTGATTTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 507
DB CGGCTTCCCGGCTCCGCTACCTGCTGATTTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 421 CAGGATGAGAGCGGCTCTCTGGGCGTGAATTTCCCTGACAGAGAGAGAGAGAGAGAGAGAG 480
DB CAGGATGAGAGCGGCTCTCTGGGCGTGAATTTCCCTGACAGAGAGAGAGAGAGAGAGAGAG 567
QY 508 CAGGATGAGAGCGGCTCTCTGGGCGTGAATTTCCCTGACAGAGAGAGAGAGAGAGAGAGAG 567
DB CAGGATGAGAGCGGCTCTCTGGGCGTGAATTTCCCTGACAGAGAGAGAGAGAGAGAGAGAG 540
QY 481 CTGGGCTGGTCTTGGCCCTCTGAGAGTGAACCCAGAGTGTACTTGAATGAGAGAGAGAGAG 540
DB CTGGGCTGGTCTTGGCCCTCTGAGAGTGAACCCAGAGTGTACTTGAATGAGAGAGAGAGAG 627
QY 541 TTCAAGGTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB TTCAAGGTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
QY 628 TTCAAGGTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
DB TTCAAGGTGAGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 601 TGGGACCACTCAGGATATTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB TGGGACCACTCAGGATATTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688
QY 688 T----- 688
DB 688 T----- 688
QY 689 ----- 688
DB 689 ----- 688
QY 721 AGGTGCTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB AGGTGCTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 781 GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
QY 689 ----- 738
DB 689 ----- 738
QY 841 AAGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB AAGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
```

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QY 901 GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
QY 799 GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
DB GAGCTGGCGGGTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 961 CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 859 CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
DB CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1021 GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
QY 919 GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
DB GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 1081 ATGGCCCGGAGATGAGCAATTTCTACCTGAGAGGCTTCACTTACCAATGTCGCGCTC 1140
DB ATGGCCCGGAGATGAGCAATTTCTACCTGAGAGGCTTCACTTACCAATGTCGCGCTC 1038
QY 979 ATGGCCCGGAGATGAGCAATTTCTACCTGAGAGGCTTCACTTACCAATGTCGCGCTC 1038
DB ATGGCCCGGAGATGAGCAATTTCTACCTGAGAGGCTTCACTTACCAATGTCGCGCTC 1200
QY 1141 TGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB TGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 1039 TGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
DB TGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1201 GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
QY 1099 GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
DB GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1261 GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1320
DB GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1218
QY 1159 GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1218
DB GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1278
QY 1321 GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1380
DB GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1278
QY 1219 GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1278
DB GCGGCGCAAGTGTGCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 1440
QY 1381 CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
QY 1279 CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
DB CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1441 GGTGGGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB GGTGGGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
QY 1303 ----- 1302
DB 1303 ----- 1560
QY 1501 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1360
QY 1303 --GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1360
DB --GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1618
QY 1561 GCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1618
DB GCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1420
QY 1361 GCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1420
DB GCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1480
QY 1421 CCATCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1480
DB CCATCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676
QY 1619 CCATCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676
DB CCATCAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
QY 1677 GCGAGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
DB GCGAGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
QY 1481 GCGAGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
DB GCGAGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1796
QY 1737 GCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1796
DB GCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600
QY 1541 GCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600
DB GCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
QY 1797 CCGGCAAGTGTGATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
DB CCGGCAAGTGTGATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660
QY 1601 CCGGCAAGTGTGATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660
DB CCGGCAAGTGTGATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
QY 1857 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
DB CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720
QY 1661 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720
DB CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976
QY 1917 CAGGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976
DB CAGGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780
```


DE Novel human coding sequence SEQ ID NO: 243.

XX Human, anti-anemic; vulnereary; anti-inflammatory; immunomodulator;
 KW anti-infectivity; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
 KW neuroprotective; anti-Parkinsonian; protein therapy; EST;
 KW expressed sequence tag; gene; ss.

OS Homo sapiens.

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The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the invention.

Sequence 2061 BP; 415 A-672 C; 605 G; 369 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 851; DB 24; Length 2061;
 Pred. No. 1.4e-170;
 Matches 851; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCTGCTCAACAGGAGCGTGGCCCGGGGAGGCGGCTCCACGCGCGGGG 60
 DB 147 ATGGCCCTGCTCAACAGGAGCGTGGCCCGGGGAGGCGGCTCCACGCGCGGGG 206
 QY 61 CCCTGGAGCCAGGCGGTCCAGCAGAGAGTGAAGTCCAGGAGGAGGAGCTTGGCGT 120
 DB 207 CCCTGGAGCCAGGCGGTCCAGCAGAGAGTGAAGTCCAGGAGGAGGAGCTTGGCGT 266
 QY 121 CTCCGGGGGCTGTCTCTGGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 DB 267 CTCCGGGGGCTGTCTCTGGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 326
 QY 181 AGTTCTGAGCAACAGAGAGGCGCGAGTGAAGAGAGTCCACGCGGAGCAGAGAGAG 240
 DB 327 AGTTCTGAGCAACAGAGAGGCGCGAGTGAAGAGAGTCCACGCGGAGCAGAGAGAG 386
 QY 241 TTGGGGGAGAGATCCAGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 387 TTGGGGGAGAGATCCAGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
 QY 301 ATGGTACAGCTGCTGAGAGCGGAGAGATGACATCCGCTGGAGCCGAGCTGAGAGAGAG 360
 DB 447 ATGGTACAGCTGCTGAGAGCGGAGAGATGACATCCGCTGGAGCCGAGCTGAGAGAGAG 506
 QY 361 CGGCTTCCCGGCTCCGCTACCTGCTGAGTGTTCATACAGAGAGAGAGAGAGAGAG 420

DB 507 CGGCTTCCCGGCTCCGCTACCTGCTGAGTGTTCATACAGAGAGAGAGAGAGAGAGAG 566
 QY 421 CAGAGTGAAGAGCTGCTCTCTGGAGGCTGAGATTTCTCTTACAGAGAGCTCCCGAGCTGAGAC 480
 DB 567 CAGAGTGAAGAGCTGCTCTCTGGAGGCTGAGATTTCTCTTACAGAGAGCTCCCGAGCTGAGAC 626
 QY 481 CTGGGCGCTGAGCTGCTGCTGAG 540
 DB 627 CTGGGCGCTGAGCTGCTGCTGAG 686
 QY 541 TTCAAGCTGAGCTGCTGCTGAG 600
 DB 687 TTCAAGCTGAGCTGCTGCTGAG 746
 QY 601 TTGGGCGAGCTGCTGCTGAG 660
 DB 747 TTGGGCGAGCTGCTGCTGAG 806
 QY 661 CCGGAGTGAAGCTGCTGCTGAG 720
 DB 807 CCGGAGTGAAGCTGCTGCTGAG 866
 QY 721 AGCTGCTGCTGCTGCTGAG 780
 DB 867 AGCTGCTGCTGCTGCTGAG 926
 QY 781 GAGCTGCTGCTGCTGCTGAG 840
 DB 927 GAGCTGCTGCTGCTGCTGAG 986
 QY 841 AAAGTGTGGA 951
 DB 987 AAAGTGTGGA 997

RESULT 11
 AAH14722
 ID AAH14722 standard; cDNA; 1755 BP.
 XX AAH14722;
 AC
 XX
 DT 26-JUN-2001 (first entry)
 DE Human cDNA sequence SEQ ID NO:12452.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-018776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

XX Claim 8; SEQ ID 12452; 2537bp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB32446 to
 CC AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 1755 BP; 350 A; 577 C; 505 G; 323 T; 0 other;

XX Query Match 35.1%; Score 694; DB 22; Length 1755;
 XX Best Local Similarity 89.1%; Pred. No. 2.2e-137;
 XX Matches 802; Conservative 0; Mismatches 0; Indels 98; Gaps 1;

QY 1081 ATGCGCCCGGAGATTGACAACTTCACTGAGCCCTTACCTACCAATGTGGCCTC 1140
 DB 322 ATGCGCCCGGAGATTGACAACTTCACTGAGCCCTTACCTACCAATGTGGCCTC 381
 QY 1141 TGGGATGAGAGTGGCGCCGAGCTGCTGCGGCACTGGAAGAGAGACACCGCTTCACTGAG 1200
 DB 382 TGGGATGAGAGTGGCGCCGAGCTGCTGCGGCACTGGAAGAGAGACACCGCTTCACTGAG 441
 QY 1201 GCTGCAAGAGCAAGAGGACCCACAGTGTCTGTCTCACTGCAAGATGGGCGTCA 1260
 DB 442 GCTGCAAGAGCAAGAGGACCCACAGTGTCTGTCTCACTGCAAGATGGGCGTCA 501
 QY 1261 GGGGCGACAGTGTGGCTTATGCAATGAGAGGATGAGAGGCTGAGAGGCGCTG 1320
 DB 502 GGGGCGACAGTGTGGCTTATGCAATGAGAGGATGAGAGGCTGAGAGGCGCTG 561
 QY 1321 CGCCAGTGCAGAGAGTCCGCGCCCATGCGCCGCCCAACCTTGGCTTCTGCGCCAGCTG 1380
 DB 562 CGCCAGTGCAGAGAGTCCGCGCCCATGCGCCGCCCAACCTTGGCTTCTGCGCCAGCTG 621
 QY 1381 CAGATCTACAGAGGCACTCTGACGGGCGACCGCCAGAGCATGTCTGGAGCAAAAATG 1440
 DB 622 CAGATCTACAGAGGCACTCTGACG----- 645
 QY 1441 GGTGGGGTCTCCCGAGAGAGACCCAGCCCTGAAGTCTTACACCAATTCACACTCTT 1500
 DB 646 ----- 645
 QY 1501 CCGCCAGAACTGAGGGTGTGGGAGAGAAAGTTGTAGGATGAAAGAGCCAGGCA 1560
 DB 646 --GCCAGAACTGAGGGTGTGGGAGAGAAAGTTGTAGGATGAAAGAGCCAGGCA 703
 QY 1561 GCCCGAAAGAGAGCTGGCGCCAGCGCACTATAAACCCTCGAGGGGTCTATGAGTCC 1620
 DB 704 GCCCGAAAGAGAGCTGGCGCCAGCGCACTATAAACCCTCGAGGGGTCTATGAGTCC 763
 QY 1621 ATCAGTCTTCTGAGAGCCCTCTTGAAGCTGAGAGAGCACTGAGAGCAAGTACATGCA 1680
 DB 764 ATCAGTCTTCTGAGAGCCCTCTTGAAGCTGAGAGAGCACTGAGAGCAAGTACATGCA 823
 QY 1681 GAGGTCTTCTTCCACAGAGTCTTCACTGAAGAGCCCTTGCAGCCCTTCCACAGCTT 1740

DB 824 GAGGTCTTCTTCCACAGAGTCTTCACTGAAGAGCCCTTGTGAGCCCTTCCACAGCTT 883
 QY 1741 GCAGAGACCAAGGAGGAGCCAGAGGTGAGCAGGAGGAGCCCTGAGCCCTGAAAGTCCGC 1800
 DB 884 GCAGAGACCAAGGAGGAGCCAGAGGTGAGCAGGAGGAGCCCTGAGCCCTGAAAGTCCGC 943
 QY 1801 CAGTCAAGTGTTCCTCTCCAGAGGCACTGCGGTGTGGCCAAACCGGACCGAGGCTTTCAG 1860
 DB 944 CAGTCAAGTGTTCCTCTCCAGAGGCACTGCGGTGTGGCCAAACCGGACCGAGGCTTTCAG 1003
 QY 1861 GAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
 DB 1004 GAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1063
 QY 1921 TTCCGAGAGGTGTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980
 DB 1064 TTCCGAGAGGTGTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1123

RESULT 12
 ABL40801
 ID ABL40801 standard; DNA; 1755 BP.
 AC ABL40801;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 XX Human MAP kinase phosphatase-1-like enzyme DNA fragment.
 XX Mitogen activated protein; MAP; MAP kinase phosphatase-1-like enzyme;
 KW antiasthmatic; antidiabetic; anorectic; cytoprotective; cardiant; human;
 KW antiepileptic; antineoplastic; antiparkinsonian; cerebroprotective; neuroprotective; nootropic; gene;
 KW neuroleptic; anticonvulsant; anti-HIV; antiarrhythmic; hypotensive;
 KW antiallergic; dermatological; vulnerary; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO2002020732-A2
 XX PD 14-MAR-2002.
 XX PF 27-AUG-2001; 2001WO-EP09848.
 XX PR 07-SEP-2000; 2000US-230709P.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Liou J;
 XX WPI; 2002-339802/37.
 XX
 PT New human mitogen activated protein kinase phosphatase-1-like enzyme
 PT polypeptide, regulators of which are useful for preventing, treating
 PT allergies including asthma, diabetes, obesity, cancer and
 PT cardiovascular diseases
 PT
 XX
 PS Disclosure; Fig 4; 134pp; English.
 XX
 CC The invention relates to a purified human mitogen activated protein (MAP)
 CC kinase phosphatase-1-like enzyme polypeptide. The enzyme can be expressed
 CC by standard recombinant methodology. The MAP kinase phosphatase-1-like
 CC enzyme and encoding polynucleotides are useful for screening for
 CC modulators which are used for treating a MAP kinase phosphatase-1-like
 CC enzyme dysfunction related disease, such as asthma, a central nervous
 CC system disorder, diabetes, obesity, chronic obstructive pulmonary
 CC disease, cancer or a cardiovascular disease. The enzyme can be regulated
 CC to treat allergies including asthma, allergic rhinitis, atopic
 CC dermatitis, and anaphylaxis, central nervous system disorders such as
 CC brain injuries, Parkinson's disease, dementia, multiple sclerosis,
 CC stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's
 CC disease, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human
 CC immunodeficiency virus (HIV) dementia, and cardiovascular diseases

387 GGTAGTTTCTACACGAGAGGAGGTTCTGAGCCAGGATGAGACGGTCTCTGGCGT 446

Search completed: January 15, 2004, 15:28:15
Job time : 545 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 13:13:53 Search time 7060 Seconds

(without alignments)
11473.238 Million cell updates/sec

Title: US-09-955-732-1

Perfect score: 1980

Sequence: 1 atggcctgtcacagtgag.....gagagggagggcgagcctga 1980

Scoring table:

IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:
2: gb_hcg:
3: gb_in:
4: gb_on:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_ov:
22: em_or:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_hcg_hum:
31: em_hcg_hum:
32: em_hcg_hum:
33: em_hcg_mus:
34: em_hcg_pln:
35: em_hcg_rtd:
36: em_hcg_mam:
37: em_hcg_vrt:
38: em_hcg_hum:
39: em_hcg_mus:
40: em_hcg_hum:
41: em_hcg_hum:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1980 | 100.0 | 1980 | 6 | AX451343 Sequence |
| 2 | 1978.4 | 99.9 | 2781 | 6 | AX099939 Sequence |
| 3 | 1978.4 | 99.9 | 2808 | 6 | AK074432 Homo sapi |
| 4 | 1978.4 | 99.9 | 2852 | 6 | AK574786 Sequence |
| 5 | 1804.8 | 91.2 | 2905 | 6 | AK094226 Homo sapi |
| 6 | 1774 | 89.6 | 2704 | 6 | AX574785 Sequence |
| 7 | 1774 | 89.6 | 2704 | 6 | AX574791 Sequence |
| 8 | 1772.4 | 89.5 | 2604 | 6 | AB072360 Homo sapi |
| 9 | 1684 | 85.1 | 2322 | 6 | AX388774 Sequence |
| 10 | 1409 | 71.2 | 1416 | 6 | AX451362 Sequence |
| 11 | 1345.6 | 68.0 | 2540 | 6 | AX574787 Sequence |
| 12 | 1292.6 | 65.3 | 2736 | 10 | BC028922 Mus muscu |
| 13 | 1153.4 | 58.3 | 1905 | 9 | BC004210 Homo sapi |
| 14 | 1153.4 | 58.3 | 1905 | 9 | BC004210 Homo sapi |
| 15 | 1026 | 51.8 | 1026 | 6 | AX086034 Sequence |
| 16 | 851 | 43.0 | 2061 | 6 | AX405828 Sequence |
| 17 | 851 | 43.0 | 2061 | 6 | AK000522 Homo sapi |
| 18 | 694 | 35.1 | 1755 | 6 | AX387678 Sequence |
| 19 | 694 | 35.1 | 1755 | 6 | BD156714 Primer fo |
| 20 | 694 | 35.1 | 1755 | 6 | AK001790 Homo sapi |
| 21 | 491 | 24.8 | 599 | 6 | AX388772 Sequence |
| 22 | 397 | 20.1 | 409 | 6 | AX388771 Sequence |
| 23 | 372 | 18.8 | 173052 | 6 | AP001885 Homo sapi |
| 24 | 362 | 18.3 | 2280 | 9 | AB072356 Homo sapi |
| 25 | 362 | 18.3 | 2433 | 9 | AK095421 Homo sapi |
| 26 | 362 | 18.3 | 3817 | 9 | AB072355 Homo sapi |
| 27 | 362 | 18.3 | 6374 | 6 | AX180874 Sequence |
| 28 | 356.4 | 18.0 | 494 | 6 | AX388773 Sequence |
| 29 | 340.4 | 17.2 | 1949 | 6 | AX223960 Sequence |
| 30 | 329 | 16.6 | 426 | 6 | AX388765 Sequence |
| 31 | 319.2 | 16.1 | 3209 | 10 | BC046529 Mus muscu |
| 32 | 308.8 | 15.6 | 1711 | 6 | AX223964 Sequence |
| 33 | 306.8 | 15.5 | 1796 | 9 | AB072358 Homo sapi |
| 34 | 300.8 | 15.2 | 3488 | 6 | AX406972 Sequence |
| 35 | 293.6 | 14.8 | 4417 | 3 | AB036834 Drosophi |
| 36 | 282.8 | 14.3 | 2260 | 6 | AX180876 Sequence |
| 37 | 279.4 | 14.1 | 1771 | 6 | AX202239 Sequence |
| 38 | 256.8 | 13.0 | 258710 | 2 | AC135823 Rattus no |
| 39 | 233.4 | 11.8 | 571 | 6 | BD149049 Primer fo |
| 40 | 231.8 | 11.7 | 302961 | 2 | AC140073 Mus muscu |
| 41 | 204 | 10.3 | 1052 | 6 | AX223966 Sequence |
| 42 | 193 | 9.7 | 92967 | 2 | AC139555 Homo sapi |
| 43 | 193 | 9.7 | 92967 | 2 | AC139555 Homo sapi |
| 44 | 142.8 | 7.2 | 386 | 9 | AF484838 Homo sapi |
| 45 | 142 | 7.2 | 113474 | 2 | AC013932 Drosophi |

ALIGNMENTS

| RESULT 1 | LOCUS | AX451343 | 1980 bp | DNA | linear | PAT 03-JUL-2002 |
|------------|------------|---|---------|-----|--------|-----------------|
| AX451343 | DEFINITION | Sequence 1 from Patent WO0224740. | | | | |
| AX451343 | ACCESSION | AX451343 | | | | |
| AX451343.1 | VERSION | GI:21698394 | | | | |
| AX451343.1 | KEYWORDS | | | | | |
| AX451343.1 | SOURCE | | | | | |
| AX451343.1 | ORGANISM | Homo sapiens (human) | | | | |
| AX451343.1 | REFERENCE | Homo sapiens | | | | |
| AX451343.1 | AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| AX451343.1 | TITLE | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AX451343.1 | JOURNAL | Lucas, R.W. and Wei, B. | | | | |
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CEPlyr, Inc. (US)
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RESULT 2
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 LOCUS Sequence 21 from Patent WO0120004.
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 ACCESSION AX099939
 VERSION AX099939.1 GI:13538949
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS Yue,H.; Tang,Y.T.; Bandman,O.; Hillman,J.L.; Baughn,M.R.,
 TITLE Azimzal,Y. and Lu,D.A.
 JOURNAL Protein phosphatase and kinase proteins
 Patent: WO 0120004-A 21 22-MAR-2001;
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| ACCESSION | AX574786 |
| VERSION | AX574786.1 GI:27551935 |
| KEYWORDS | |
| SOURCE | |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | |
| AUTHORS | Wei, M.H., Ketchum, K.A., di Francesco, V. and Beasley, E.M. |
| TITLE | Isolated human phosphatase proteins, nucleic acid molecules encoding human phosphatase proteins, and uses thereof |
| JOURNAL | Patent: WO 0242436-A 2 30-MAY-2002; |
| FEATURES | PE Corporation (NY) (US) |
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 AK094226
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 ORGANISM
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REFERENCE
 AUTHORS
 1 Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Matsuma, M., Miyakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Iisogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2905)

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Iisogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Iisogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kametani, Kisarazu, Chiba 292-0812, Japan
 E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-, 3'- and one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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ORIGIN

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374 GCAAGGATCCCAAGTCCCAAG 433
306 ACAAGCTGAG 365
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426 TGAGAGCGTCTCTGAG 461
554 TGAGAGCGTCTCTGAG 613
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467 CCCCAGCTGACAGCTGAG 526
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1994 CCTTAAATCCCGAG 2053
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2114 CCTTAAAG 2173
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2174 AAG

RESULT 6

AX574785 LOCUS AX574785 2704 bp DNA linear PAT 07-JAN-2003
 DEFINITION Sequence 1 from Patent WO242436.
 AX574785
 ACCESSION
 VERSION AX574785.1 GI:27551934
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
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 AUTHORS Wei, M.H., Ketchum, K.A., di Francesco, V., and Beasley, E.M.
 TITLE Isolated human phosphatase proteins, nucleic acid molecules
 encoding human phosphatase proteins, and uses thereof
 JOURNAL Patent: WO 02/2436-A 1 30-May-2002;
 PE Corporation (NY) (US)
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 Best Local Similarity 95.1%; Pred. No. 0;
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| Db | 1736 | GCAAGACCAAGGAGGCGCAGAGGTGGACAAGGGGGCTCACGCCTGACGAATGCCG | 1735 |
| Oy | 1801 | CAGTCAGAGTAAACCTCCAGGGCATGCCCCGGTGAGCAACCAGGACTTTCCAG | 1866 |
| Db | 1796 | CAGTAGAGTTAACCCTCCAGGGCATGCCCCGGTGAGCAACCAGGACTTTCCAG | 1855 |
| Oy | 1861 | GAGCAGACAGAGGGCAGGGGACAGGGAGAGAGCCCTGATTCTCTACGCCACAG | 1920 |
| Db | 1856 | GAGCAGACAGAGGGCAGGGGACAGGGAGAGAGCCCTGATTCTCTACGCCACAG | 1915 |
| Oy | 1921 | TTCCGGAAGGTGGTGAACAAGGCCAGCGTGCATGCACTGGAGAAGAGGGCGAGGCTTGA | 1988 |
| Db | 1916 | TTCCGGAAGGTGGTGAACAAGGCCAGCGTGCATGCACTGGAGAAGAGGGCGAGGCTTGA | 1975 |
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| LOCUS | Sequence 7 from Patent WO0242436. | | |
| DEFINITION | AX574791 | | |
| ACCESSION | AX574791.1 GI:27551937 | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | Weil,M.H., Ketchum,K.A., di Francesco,V. and Beasley,E.M. | | |
| JOURNAL | Isolated human phosphatase proteins, nucleic acid molecules encoding human phosphatase proteins, and uses thereof Patent: WO 0242436-A 7 30-MAY-2002; PE Corporation (NY) (US); Location/Qualifiers 1..2704 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" | | |
| FEATURES | | | |
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| Oy | 61 | CCCTGGGACCAAGGCGGTCACAGGAAGGTGACATCCACGGAAGCAGAGCTTTGCGGTG | 120 |
| Db | 154 | CCCTGGGACCAAGGCGGTCACAGGAAGGTGACATCCACGGAAGCAGAGCTTTGCGGTG | 213 |
| Oy | 121 | CTCCGTGGGGGTGCTGCTCGGACCTGAGATGAGAGGGGACAATGATGATGACAGAGGCC | 180 |
| Db | 214 | CTCCGTGGGGGTGCTGCTCGGACCTGAGATGAGAGGGGACAATGATGATGACAGAGGCC | 273 |
| Oy | 181 | AGTTTGAGCCACAAGAAAGGCCCCCGAGTGAAGAGAGCTTCAAGGGGACCAAGACAAG | 240 |
| Db | 274 | AGTTTGAGCCACAAGAAAGGCCCCCGAGTGAAGAGAGCTTCAAGGGGACCAAGACAAG | 333 |
| Oy | 241 | TTCCGGGCAAGGATCCCAGAGTCCCAGAGAAGCAGAGAGCAGAGGACAGACTTGCACCTC | 300 |
| Db | 334 | TTCCGGGCAAGGATCCCAGAGTCCCAGAGAAGCAGAGAGCAGAGGACAGACTTGCACCTC | 393 |
| Oy | 301 | ATGTGACAGCTGCTGAGGCGCGCAGGATGACATCGCCTTGGCAGGCCCAAGCTGAGGACCC | 360 |
| Db | 394 | ATGTGACAGCTGCTGAGGCGCGCAGGATGACATCGCCTTGGCAGGCCCAAGCTGAGGACCC | 453 |
| Oy | 361 | CGGCTCCCCCGGCTCCGCTACTGCTGGAGTTTTCACACGAGAGAGAGAGTCTTGAGC | 420 |
| Db | 454 | CGGCTCCCCCGGCTCCGCTACTGCTGGAGTTTTCACACGAGAGAGAGAGTCTTGAGC | 513 |
| Oy | 421 | CAGGATGAGACGCTCCTCGGGCGGTGATTTTCCTGACAGCAGCTCCCCAGCTGAC | 480 |

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| Db | 514 | CAGGATGAGACGAGCTCTCCCTGGGGGTGGATTTCCTCTGACAGACAGCTCCCCAGCTGACC | 573 |
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| Db | 574 | CTGGGCGCTGGCTTTGGCCCTCTGGAGTGAACACCAGGTGTACTTAAATGGAGAGCGGGGCG | 633 |
| Oy | 541 | TTTCAGCTGACATGTGGTGGGGCAAAAGCCGATCTTCAAGCCATCTCATTCAGACCATG | 600 |
| Db | 634 | TTTCAGCTGACATGTGGTGGGGCAAAAGCCGATCTTCAAGCCATCTCATTCAGACCATG | 693 |
| Oy | 601 | TGGGCACTACTCCAGGTATTGCAACAGCATGTGAGGCACTCTAAGGCAAGCGGCTTTGTA | 660 |
| Db | 694 | TGGGCACTACTCCAGGTATTGCAACAGCATGTGAGGCACTCTAAGGCAAGCGGCTTTGTA | 753 |
| Oy | 661 | CCGGGTGGCAATGACCTCACCTGGGCGAGCCATACAGAGAGACTGAATCTCCGAACAG | 720 |
| Db | 754 | CCGGGTGGCAATGACCTCACCTGGGCGAGCCATACAGAGAGACTGAATCTCCGAACAG | 813 |
| Oy | 721 | AGCTGCTCAATGATGAGAGGCTAATGAGCCGACCTGGAGTCTCTGCGGCTCCAGCGCC | 780 |
| Db | 814 | AGCTGCTCAATGATGAGAGGCTAATGAGCCGACCTGGAGTCTCTGCGGCTCCAGCGCC | 873 |
| Oy | 781 | GAGCTGTGGCGGTCTCTAGAAACAGGAGCATGAGAGCGAGATCCGTGTCTGAGCTGTGG | 840 |
| Db | 874 | GAGCTGTGGCGGTCTCTAGAAACAGGAGCATGAGAGCGAGATCCGTGTCTGAGCTGTGG | 933 |
| Oy | 841 | AAAGTGTGATGTCAATGACCTGGAAGATGTCACTTCCAAAGAGATCCGCAAGCTGTG | 900 |
| Db | 934 | AAAGTGTGATGTCAATGACCTGGAAGATGTCACTTCCAAAGAGATCCGCAAGCTGTG | 993 |
| Oy | 901 | GAGCTGTGGCGGTCTCTAGAAACAGGAGCATGAGAGCGAGATCCGTGTCTGAGCTGTGG | 960 |
| Db | 994 | GAGCTGTGGCGGTCTCTAGAAACAGGAGCATGAGAGCGAGATCCGTGTCTGAGCTGTGG | 1053 |
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| Db | 1054 | CTGCTGGTGGCACAACCGGGAACCGAGCCTCCCGGATCTTCCCGCACTCTACCTGGGCTCA | 1113 |
| Oy | 1021 | GAGTGAACAGCAGCAAACTGTGAGAGACTGTGAGAGAAACAGGAGTACCCACATCTTGAAC | 1080 |
| Db | 1114 | GAGTGAACAGCAGCAAACTGTGAGAGACTGTGAGAGAAACAGGAGTACCCACATCTTGAAC | 1173 |
| Oy | 1081 | ATGAGCCCGGGAGATTGACAACTTACCTGAGGGCTTACCTACCAATGATGCGCTCT | 1140 |
| Db | 1174 | ATGAGCCCGGGAGATTGACAACTTACCTGAGGGCTTACCTACCAATGATGCGCTCT | 1233 |
| Oy | 1141 | TGGATATGAGAGTGGGCCCAAGCTCTGCGCATGTGAAGAGAGCAACCGTTATTGAG | 1200 |
| Db | 1234 | TGGATATGAGAGTGGGCCCAAGCTCTGCGCATGTGAAGAGAGCAACCGTTATTGAG | 1293 |
| Oy | 1201 | GCTCCAAAGACACAGGGCACTCCACGTGTGTCCACTGTCAAGATGGGGCTGATGCGCTCA | 1260 |
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| Oy | 1261 | GCGGCCACAGTGGTGGGCTTATGCCATGAAGAGTAAACAAATGACAGCTGGAGCAGGCTGT | 1320 |
| Db | 1354 | GCGGCCACAGTGGTGGGCTTATGCCATGAAGAGTAAACAAATGACAGCTGGAGCAGGCTGT | 1413 |
| Oy | 1321 | CGCCACGTGACAGAGCTCCCGGCCCATGCGCCGCCCAACCTGTGCTTTCTGCGCAAGCTG | 1380 |
| Db | 1414 | CGCCACGTGACAGAGCTCCCGGCCCATGCGCCGCCCAACCTGTGCTTTCTGCGCAAGCTG | 1473 |
| Oy | 1381 | CAGATCTAACAGGGGCACTCTGACGGGCCACCGCCAGAGCCATGTCTGGAGACCAAAATGT | 1440 |
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| Oy | 1441 | GGTGGGCTCTCCCAAGAGAGCAACCAGCCCTGAAGTCTCTACACCAATCCACCTCTT | 1500 |
| Db | 1498 | ----- | 1497 |
| Oy | 1501 | CCGCCAGAACTTAGGGGTGGTGGGAGAGAAAGTTGTAGGCATGGAAGAGACCGCAGCA | 1566 |

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| QY | 841 | AAAGGTGTGATGTCAAGTACCTGTGGAGATGTCACTTCCAAAGAGATCCGACAGCTCTG | 900 |
| Db | 841 | AAAGGTGTGATGTCAAGTACCTGTGGAGATGTCACTTCCAAAGAGATCCGACAGCTCTG | 900 |
| QY | 901 | GAGCTTCGCTGTGGAGCTCCCTCCAGCAGTACCGTAGCTTCATGCACCAACAGATGCTG | 960 |
| Db | 901 | GAGCTTCGCTGTGGAGCTCCCTCCAGCAGTACCGTAGCTTCATGCACCAACAGATGCTG | 960 |
| QY | 961 | CTGCTGTGTGGCAACAGGGGACCGAGGCTCCGCATCTTCCCACTTCACTTACCTGGAGCTA | 1020 |
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| Db | 1321 | CGCCACGTGCAGAGAGCTCCGGGCCATCGCCCGCCCAACCTGTGGCTTCTGTGCCAGCTG | 1380 |
| QY | 1381 | CAGATCTTACCAAGGAGATCTGTAGCGGCCAGCGCCAGAGCATGTCTGGAGAGAGAAATG | 1440 |
| Db | 1381 | CAGATCTTACCAAGGAGATCTGTAGCGGCCAGCGCCAGAGCATGTCTGGAGAGAGAAATG | 1440 |
| QY | 1441 | GGTGGGGTCTCCCCAGAGAGAGACCAAGCCCTGAAATCTTACACCAATCCCACTCTT | 1500 |
| Db | 1405 | ----- | 1405 |
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| Db | 1405 | --GCCAGAACTGAGGGGTGTGGGAGGAGAAAGTTGTATGCGATGGAAGAGACCAAGCA | 1462 |
| QY | 1561 | GCCCCGAAGAAAGACCTGTGGGCGACAGGCCATTTAAACCTCGAGGGGCTCATGAGTCTC | 1620 |
| Db | 1463 | GCCCCGAAGAAAGACCTGTGGGCGACAGGCCATTTAAACCTCGAGGGGCTCATGAGTCTC | 1522 |
| QY | 1621 | ATCAGTCTTCTGAGACCCCTCCTTGGAGCTTGAGAGCACTCTGAGAGCAAGTATGCA | 1680 |
| Db | 1523 | ATCAGTCTTCTGAGACCCCTCCTTGGAGCTTGAGAGCACTCTGAGAGCAAGTATGCA | 1582 |
| QY | 1681 | GAGGTCTTCTCTTCCCAAGAGCTTCAACATGAAGAGCTGTGACAGCTTCCCAAGACTT | 1740 |
| Db | 1583 | GAGGTCTTCTCTTCCCAAGAGCTTCAACATGAAGAGCTTGTGACAGCTTCCCAAGACTT | 1642 |
| QY | 1741 | GCAAGACCAAGGAGGCGCAGCAGGTGGAACAGGGGGCTCAGCCTGACCTTGAAATGCCG | 1800 |
| Db | 1643 | GCAAGACCAAGGAGGCGCAGCAGGTGGAACAGGGGGCTCAGCCTGAGATGCCG | 1702 |
| QY | 1801 | CAGTACAGTGTTAACCTTCCAGGGCAGTGCCTGTGTGGCCAAACCGAACCCAGGCTTCCAG | 1860 |
| Db | 1703 | CAGTACAGTGTTAACCTTCCAGGGCAGTGCCTGTGTGGCCAAACCGAACCCAGGCTTCCAG | 1762 |
| QY | 1861 | GAGCAGAGACAGGGGCGACAGGGGACAGGGGACAGGAGACCTTGATTTCTCTTACGCCACAG | 1920 |
| Db | 1763 | GAGCAGAGACAGGGGCGACAGGGGACAGGGGACAGGAGACCTTGATTTCTCTTACGCCACAG | 1822 |
| QY | 1921 | TTCCGAAAGGTGTGAGACAGGCGTGCATGAACGTGAGAGAGAGGGCGAGGCTTGA | 1980 |

| DB | 1823 | TTCCGGAAGTGGTGGAGCAGCCAGCGTGCATACAGTGGAGAGAGCGCGAGCCTGA | 1882 |
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| RESULT 9 | AX398774 | 2322 bp | DNA |
| LOCUS | AX398774 | | linear |
| DEFINITION | Sequence 10 from Patent WO0202732. | | PAT 27-MAY-2002 |
| ACCESSION | AX398774 | | |
| VERSION | AX398774.1 | GI:21261307 | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| JOURNAL | Regulation of human map kinase phosphatase-like enzyme | | |
| FEATURES | Patent: WO 020732-A 10 14-MAR-2002; | | |
| source | Bayer Aktiengesellschaft (DE) | | |
| location/Qualifiers | 1..2322 | | |
| BASE COUNT | 467 a 751 c 718 g 386 t | | |
| ORIGIN | | | |
| Query Match | 85.1%; Score 1684; DB 6; Length 2322; | | |
| Best Local Similarity | 95.0%; Pred. No. 2.6e-307; | | |
| Matches 1852; Conservative | 0; Mismatches 75; Indels 23; Gaps 10; | | |
| 39 | CGCGCGCTCCACGCGCGTGGGCCCCCTGGAGACCAAGCGGTCCAGCGAAGAGTGCATCCA | 98 | |
| 147 | CGCCCTACCCCTGGGGGTGCTCTCTCGGACAGACCTGTCCAGGAAGAGTGCATCCA | 206 | |
| 99 | CGGAAGGCAGAGCTTTGGGTGCTCC-GTGGGGCTGTCTTGGACTGACAGATGGAGGG | 157 | |
| 207 | GCGA----AGAGCTTTGGGTGCTCTGTGGGGGTGCTCTGGGACTGAGAGTGAAGGG | 262 | |
| 158 | ACATATGATGATGACAGAGAGGCGCATCTGTGAGCCAAAGAGAGAGCCCGAGTAGAGG | 217 | |
| 263 | ACATATGATGATGACAGAGAGGCGCATCTGTGAGCCAAAGAGAGAGCCCGAGTAGAGG | 322 | |
| 218 | AGCTCCACGGG--ACCAACAGACTT--CGGCAAGATCCCAAGTCCCGAAGACA | 272 | |
| 323 | AGCTCCACGGGAGAACCCAGACACACTTTCGTGACAGATCCCAAGTCCCGAAGACA | 382 | |
| 273 | GGAGGAGAGAGGAGAGACCTGACCTCATGTGACGTGAGGCGCGAGATGACAT | 332 | |
| 383 | GGAGGAGAGAGGAGAGACCTGACCTCATGTGAGGCGCGAGATGACAT | 442 | |
| 333 | CGGCGTGGCA--GGCCAGCTGGAGGCAACCCCGGCTCCCGGCTCCGCTACCTGC---- | 385 | |
| 443 | CGGCGTGGCA--GGCCAGCTGGAGGCAACCCCGGCTCCCGGCTCCGCTACCTGC | 502 | |
| 386 | TGGATGATTTCTACACGAGAA--GAGAGAGTCTGAG--CCAGATAGAGCGGTCTCGGG | 443 | |
| 503 | TGGATGATTTCTACACGAGAGGAGAGAGTCTGAGCCAGATAGAGCGGTCTCGGG | 562 | |
| 444 | -CGTGAATTTCCCTGACAGAGAGCTCCCGGCTGGACCTTGAGGCTGTCTTGGCCCTCT | 502 | |
| 563 | ACGTGATTTCCCTGACAGAGAGCTCCCGGCTGGACCTTGAGGCTGTCTTGGCCCTCT | 622 | |
| 503 | GGATGACACCCAGGTGACTTGAATGAGAACGGGGGCTTCAAGGTACGCTGTGTGGGC | 562 | |
| 623 | GGATGACACCCAGGTGACTTGAATGAGAACGGGGGCTTCAAGGTACGCTGTGTGGGC | 682 | |
| 563 | AAACCCGATTTTCAACCCCATCTCCATTCAGACACATGTGGGCACACTCCAGTATTGC | 622 | |
| 683 | AAACCCGATTTTCAACCCCATCTCCATTCAGACACATGTGGGCACACTCCAGTATTGC | 742 | |
| 623 | ACCAAGATGAGGAGAGCTTGAAGAGCGGCGCTTGAACGGGTGCAATGCCCTCACT | 682 | |

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Db      743 ACCAAGCATGTAGAGAGCTCTAGGAGAGGAGGCTTGTATCCGGGTGAGAGTCCCTCACT 802
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Db      803 GGGCCAGCCACTACAGAGAGACTGAACTCCGAACAGAGTCCCTCAATGATGAGAGG 862
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REFERENCE          1 Luche, R.M. and Wei, B.
AUTHORS            Dsp-15 dual-specificity phosphatase
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DEFINITION Sequence 3 from Patent WO0242436.
ACCESSION AX574787
VERSION AX574787.1 GI:27551936
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1 Wei, M.H., Ketchum, K.A., di Francesco, V., and Beasley, E.M.
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 AUTHORS Strausberg, R.
 TITLE Direct Submission
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 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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 Email: cgabbs-remail.nih.gov
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 DB 665 GAAGCTCTTACACCATTCCTCCCTCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
 QY 1534 GTTGTAGCATGAG 1593
 DB 725 GTTGTAGCATGAG 784
 QY 1594 ATAAACCTCCAGAGGAGTATAGAGTCAATCACTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1653
 DB 785 ATAAACCTCCAGAGGAGTATAGAGTCAATCACTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 844
 QY 1654 AGCAGCTCAG 1713
 DB 845 AGCAGCTCAG 904
 QY 1714 GAGCTCTGAG 1773
 DB 905 GAGCTCTGAG 964
 QY 1774 GGGCTCTGAG 1833
 DB 965 GGGCTCTGAG 1024
 QY 1834 GTGAGCAACCGAG 1893
 DB 1025 GTGAGCAACCGAG 1084
 QY 1894 GAGCCCTCATTTCTTACAGCCAGGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1953

| | | | |
|----|------|--|------|
| QY | 24 | TTCCGGCAGAGATCCCACAGTCCCGAAGAAGGAGAGACAAGGCACACTGTCACTC | 300 |
| Dp | 241 | TTCCGGCAGAGATCCCACAGTCCCGAAGAAGGAGAGACAAGGCACACTGTCACTC | 300 |
| QY | 301 | ATGATACAGCTTCCTGAGGCCGAGATACATCCGCTTGGA GCCACTGAGGACC | 360 |
| Dp | 301 | ATGATACAGCTTCCTGAGGCCGAGATACATCCGCTTGGA GCCACTGAGGACC | 360 |
| QY | 361 | CGGCTCCCCGGCTCCGCTACCTGTGTAGTTTTCACAGAAAGAGAGTCTGAGC | 420 |
| Dp | 361 | CGGCTCCCCGGCTCCGCTACCTGTGTAGTTTTCACAGAAAGAGAGTCTGAGC | 420 |
| QY | 421 | CAGATGAGACGGTCTCTTGAGGCTGGAATTTCCCTGACAGAGTCCCCAGCTGCACC | 480 |
| Dp | 421 | CAGATGAGACGGTCTCTTGAGGCTGGAATTTCCCTGACAGAGTCCCCAGCTGCACC | 480 |
| QY | 481 | CTGGGCGCTGTCTTGCCCTCTGAGTAGACCCAGGTGTACTTAATGAGAGCGGGGC | 540 |
| Dp | 481 | CTGGGCGCTGTCTTGCCCTCTGAGTAGACCCAGGTGTACTTAATGAGAGCGGGGC | 540 |
| QY | 541 | TTACAGCTGACGTCTGTGTGGCAAAGCCGATCTTAAGCCCATCTCATCACACATG | 600 |
| Dp | 541 | TTACAGCTGACGTCTGTGTGGCAAAGCCGATCTTAAGCCCATCTCATCACACATG | 600 |
| QY | 601 | TGGACCACTCCAGATATTGTACAACAACTAGTAGAGAGCTTAGAGCAGCGCTGTATA | 660 |
| Dp | 601 | TGGACCACTCCAGATATTGTACAACAACTAGTAGAGAGCTTAGAGCAGCGCTGTATA | 660 |
| QY | 661 | CCGGGTGGCAATGCCCTTCACTGGGCGACCACTAACAGAGATCTAATCCGAATG | 720 |
| Dp | 661 | CCGGGTGGCAATGCCCTTCACTGGGCGACCACTAACAGAGATCTAATCCGAATG | 720 |
| QY | 721 | AGCTGCCCAATGATGTGACGAGCTATGAGCCACCTGAGATCTCTGGGCTCCAGCGCC | 780 |
| Dp | 721 | AGCTGCCCAATGATGTGACGAGCTATGAGCCACCTGAGATCTCTGGGCTCCAGCGCC | 780 |
| QY | 781 | GAGCTGGCGGGTCTCTCAGAACAGAGAGATGAGAGCGAGATCCGTCTGACTGTGG | 840 |
| Dp | 781 | GAGCTGGCGGGTCTCTCAGAACAGAGAGATGAGAGCGAGATCCGTCTGACTGTGG | 840 |
| QY | 841 | AAATGTGTGATGTCAAGTACCTGAGAGTGTCACTTCCAAGAGATCCGCAAGCTGTG | 900 |
| Dp | 841 | AAATGTGTGATGTCAAGTACCTGAGAGTGTCACTTCCAAGAGATCCGCAAGCTGTG | 900 |
| QY | 901 | GAGCTGGCGCTTCGCCCTCCAGAGTACCGTACTTATCGACACCAATGCTG | 960 |
| Dp | 901 | GAGCTGGCGCTTCGCCCTCCAGAGTACCGTACTTATCGACACCAATGCTG | 960 |
| QY | 961 | CTGCTGTGGCAGACGGGACCGAGCCTCCCGCATCTTCCCCCACTTACTCTGGGCTCA | 1020 |
| Dp | 961 | CTGCTGTGGCAGACGGGACCGAGCCTCCCGCATCTTCCCCCACTTACTCTGGGCTCA | 1020 |
| QY | 1021 | GAGTGGAAACGACGAAACTTGGAGAGAGTGTAGAGAGAACAGGTGATCCCAATTTGAA | 1080 |
| Dp | 1021 | GAGTGGAAACGACGAAACTTGGAGAGAGTGTAGAGAGAACAGGTGATCCCAATTTGAA | 1080 |
| QY | 1081 | ATGGCCCGGAGATTGACACTTCTACCTTAGCGCTTCACTCAACATGTGCGCTC | 1140 |
| Dp | 1081 | ATGGCCCGGAGATTGACACTTCTACCTTAGCGCTTCACTCAACATGTGCGCTC | 1140 |
| QY | 1141 | TGGATATAGAGATGGCGCCAGCTGTGCGGACTGTGAAGAGAGACCGCTTATTGAG | 1200 |
| Dp | 1141 | TGGATATAGAGATGGCGCCAGCTGTGCGGACTGTGAAGAGAGACCGCTTATTGAG | 1200 |
| QY | 1201 | GCTGCAAGAGACAGGACACCACTGTGTTCACATGCAAGATGGGCGTACGCGCTCA | 1260 |
| Dp | 1201 | GCTGCAAGAGACAGGACACCACTGTGTTCACATGCAAGATGGGCGTACGCGCTCA | 1260 |
| QY | 1261 | GCGGCCACAGTCTGGGCTATGCAATAGAGAGTACAAATGACACTGTGAACAGGCTGTG | 1320 |
| Dp | 1261 | GCGGCCACAGTCTGGGCTATGCAATAGAGAGTACAAATGACACTGTGAACAGGCTGTG | 1320 |

| | | | |
|----|------|---|------|
| QY | 1321 | CGCCACGCTGACAGAGCTCCGGCCCATCGCCCGCCCAACCCCTGGCTTCTGCGCAGGTG | 1380 |
| Db | 1321 | CGCCACGCTGACAGAGCTCCGGCCCATCGCCCGCCCAACCCCTGGCTTCTGCGCAGGTG | 1380 |
| QY | 1381 | CAGATCTTACCAAGGGCATCTCTGACCGGCCAAGCCGCTGAGTCTCTACACCATTCCTT | 1440 |
| Db | 1381 | CAGATCTTACCAAGGGCATCTCTGACCGGCCAAGCCGCTGAGTCTCTACACCATTCCTT | 1440 |
| QY | 1441 | GGTGGGGCTCTCCCGAGAGAGCACCCAGCCCTCTAGCTCTTACACCATTCCTT | 1500 |
| Db | 1441 | GGTGGGGCTCTCCCGAGAGAGCACCCAGCCCTCTAGTCTCTACACCATTCCTT | 1500 |
| QY | 1501 | CCGGCAGAACCTGAGGGGTGTTGGGGAGAGAAAGTTGTATGACATGAAAGAGCCAGGCA | 1560 |
| Db | 1501 | CCGGCAGAACCTGAGGGGTGTTGGGGAGAGAAAGTTGTATGACATGAAAGAGCCAGGCA | 1560 |
| QY | 1561 | GCCCCGAAAGAAAGCCTGGGCCACCGGCCACGTATAAAGCTCCGAGGGGTCTATGAGTCC | 1620 |
| Db | 1561 | GCCCCGAAAGAAAGCCTGGGCCACCGGCCACGTATAAGCTCCGAGGGGTCTATGAGTCC | 1620 |
| QY | 1621 | ATCAGCTCTTCGAGAGCCCTCCTTGGAGCTGGAGAGCACTTCAGAGACCAAGTGCATGCA | 1680 |
| Db | 1621 | ATCAGCTCTTCGAGAGCCCTCCTTGGAGCTGGAGAGCACTTCAGAGACCAAGTGCATGCA | 1680 |
| QY | 1681 | GAGGTCTTCTCTTCCACGAGTCTTCAATGAAGAGCCTCTGACGCCCTTCCACAGCTT | 1740 |
| Db | 1681 | GAGGTCTTCTCTTCCACGAGTCTTCAATGAAGAGCCTCTGACGCCCTTCCACAGCTT | 1740 |
| QY | 1741 | GCAAGGACCAAGGAGGCGACAGTAGTGAACAGGGGGGCTCAGCTTGCCTGAAATCCGCG | 1800 |
| Db | 1741 | GCAAGGACCAAGGAGGCGACAGTAGTGAACAGGGGGGCTCAGCTTGCCTGAAATCCGCG | 1800 |
| QY | 1801 | CAGTCAAGTGGTTACCTCTCCAGGGGAGTGGCGGTGGTGGCCAAACCGGACCCAGGCTTCCAG | 1860 |
| Db | 1801 | CAGTCAAGTGGTTACCTCTCCAGGGGAGTGGCGGTGGTGGCCAAACCGGACCCAGGCTTCCAG | 1860 |
| QY | 1861 | GAGCAGAGAGCAGGGGCGAGGGGACAGGGGCAAGGAGAGCCCTGCATTTTCTCTACGCCCAGG | 1920 |
| Db | 1861 | GAGCAGAGAGCAGGGGCGAGGGGACAGGGGCAAGGAGAGCCCTGCATTTTCTCTACGCCCAGG | 1920 |
| QY | 1921 | TTCCGGAAGGTGTGTGAACACAGGCCAGGTGCTATGACAGTGGAGAGAGGGCGAGGGCTTGA | 1980 |
| Db | 1921 | TTCCGGAAGGTGTGTGAACACAGGCCAGGTGCTATGACAGTGGAGAGAGGGCGAGGGCTTGA | 1980 |

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RESULT 2
US-09-761-640-2
; Sequence 2, Application US/09761640
; Patent No. US20020137042A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00964-CIP
; CURRENT APPLICATION NUMBER: US/09/761,640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2852
TYPE: DNA
ORGANISM: Human
US-09-761-640-2

Query Match          99.9%; Score 1978.4; DB 10; Length 2852;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1979; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATGGCCCTGTGTCACAGTGCAGGCCGTTGCCCCCGAGGACGCGGCTCACCAGCCCGTAGGG 60
db      |||||
        ATGGCCCTGTGTCACAGTGCAGGCCGTTGCCCCCGAGGACGCGGCTCACCAGCCCGTAGGG 116

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QY 61 CCTGGGACACAGCGGCTCCAGGAGAGTCACTCCAGCGAAGGACAGAGCTTTGCGGTG 120
Db 117 CCTGGGACACAGCGGCTCCAGGAGAGTCACTCCAGCGAAGGACAGAGCTTTGCGGTG 176
QY 121 CTCCTGGGGCTGTCTCTGGGACTGCAAGATGGAAGGACATGATGATGACAGAGGC 180
Db 177 CTCCTGGGGCTGTCTCTGGGACTGCAAGATGGAAGGACATGATGATGACAGAGGC 236
QY 181 AGTTCTGAGCCAAACAGAAAGGCGGAGTGAAGAGAGTCCAGCGGGACACAGACAGC 240
Db 237 AGTTCTGAGCCAAACAGAAAGGCGGAGTGAAGAGAGTCCAGCGGGACACAGACAGC 296
QY 241 TTGGGCAAGATCCCAAGATCCCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 297 TTGGGCAAGATCCCAAGATCCCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356
QY 301 ATGATACAGCTGTGAGGGCGGAGAGATGACATCCGCTGGGAGAGAGAGAGAGAGAG 360
Db 357 ATGATACAGCTGTGAGGGCGGAGAGATGACATCCGCTGGGAGAGAGAGAGAGAGAG 416
QY 361 CGAGCTCCCGGCTCCGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 417 CGAGCTCCCGGCTCCGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 476
QY 421 CAGGATGAAGAGTCTCTCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 477 CAGGATGAAGAGTCTCTCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 536
QY 481 CTGGGCTGT 540
Db 537 CTGGGCTGT 596
QY 541 TTACGCTGACGCTCTGT 600
Db 597 TTACGCTGACGCTCTGT 656
QY 601 TGGGCGACACTCAGGATTTGACACAGAGATGAGGAGAGCTCTGAGGAGAGAGAGAG 660
Db 657 TGGGCGACACTCAGGATTTGACACAGAGATGAGGAGAGCTCTGAGGAGAGAGAGAG 716
QY 661 CCGGCTGGGAGTGCCTCTCACTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 717 CCGGCTGGGAGTGCCTCTCACTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776
QY 721 AACTGCTCAATGAGTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 777 AACTGCTCAATGAGTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 836
QY 781 GAGCTGCGGAGTCTCTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 837 GAGCTGCGGAGTCTCTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
QY 841 AAAGTGTGAGTGTCACTGTGAAGTGTCACTTCCAAAGAGATCCGAGAGAGAGAG 900
Db 897 AAAGTGTGAGTGTCACTGTGAAGTGTCACTTCCAAAGAGATCCGAGAGAGAGAG 956
QY 901 GAGCTGCGGAGTCTCTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 957 GAGCTGCGGAGTCTCTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1016
QY 961 CTGCTGTGTGCAACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 1017 CTGCTGTGTGCAACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
QY 1021 GAGTGAAG 1080
Db 1077 GAGTGAAG 1136
QY 1081 ATGGCCCGGAGAGATTGACAACTTTACCTGTGAGCGGTTACCTTACCAATGTGGCGCTC 1140
Db 1137 ATGGCCCGGAGAGATTGACAACTTTACCTGTGAGCGGTTACCTTACCAATGTGGCGCTC 1196
QY 1141 TGGGATGAGAGAGTGGGCGGAGAGTGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

Db 1197 TGGGATGAGAGAGTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256
QY 1201 GCTGCAAG 1260
Db 1257 GCTGCAAG 1316
QY 1261 GCGGCGCAGT 1320
Db 1317 GCGGCGCAGT 1376
QY 1321 CGCCAGCTGCAAG 1380
Db 1377 CGCCAGCTGCAAG 1436
QY 1381 CAGATCTACAG 1440
Db 1437 CAGATCTACAG 1496
QY 1441 GGTGGGAGTCTTCCCGAG 1500
Db 1497 GGTGGGAGTCTTCCCGAG 1556
QY 1501 CCGGCAAG 1560
Db 1557 CCGGCAAG 1616
QY 1561 GCCCGCAAG 1620
Db 1617 GCCCGCAAG 1676
QY 1621 ATCAGTCTTCTGAG 1680
Db 1677 ATCAGTCTTCTGAG 1736
QY 1681 GAGGCTCTTCTTCCAG 1740
Db 1737 GAGGCTCTTCTTCCAG 1796
QY 1741 GCAG 1800
Db 1797 GCAG 1856
QY 1801 CAGTCAAGT 1860
Db 1857 CAGTCAAGT 1916
QY 1861 GAGCAG 1920
Db 1917 GAGCAG 1976
QY 1921 TTCCGGAAGT 1980
Db 1977 TTCCGGAAGT 2036

RESULT 3
US-10-108-260A-74
Sequence 74, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cdna
FILE REFERENCE: HI-A0106
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 2905
TYPE: DNA
ORGANISM: Homo sapiens
US-10-108-260A-74

Query Match 91.2%; Score 1804.8; DB 12; Length 2905;
 Best Local Similarity 95.7%; Pred. No. 0;
 Matches 1909; Conservative 0; Mismatches 2; Indels 83; Gaps 2;

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QY 66 GGAACGAGCGGCTCAGACGAGAGAGTCTCCAGCGAGGAGAGAGCTTTGCGTCTCG 125
Db 198 GGAACGAGCGGCTCAGACGAGAGAGTCTCCAGCGAGAGAGCTTTGCGTCTCG 253
QY 126 TGGGGCTGTCTCGGAGCTGACAGGATGAGAGGAGCAATGATGATGAGAGAGAGGAGTTC 185
Db 254 TGGGGCTGTCTCGGAGCTGACAGGATGAGAGGAGCAATGATGATGAGAGAGGAGTTC 313
QY 186 TGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 245
Db 314 TGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 373
QY 246 GCAAGAGATCCCAAGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 305
Db 374 GCAAGAGATCCCAAGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 433
QY 306 ACAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 365
Db 434 ACAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 493
QY 366 TCCCGGAGCTCGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
Db 494 TCCCGGAGCTCGCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 553
QY 426 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 461
Db 554 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 613
QY 462 -----GAGCT 466
Db 614 GAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 673
QY 467 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 526
Db 674 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 733
QY 527 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 586
Db 734 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 793
QY 587 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 646
Db 794 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 853
QY 647 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 706
Db 854 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 913
QY 707 TGAAGCTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 766
Db 914 TGAAGCTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 973
QY 767 GAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 826
Db 974 GAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1033
QY 827 GTCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 886
Db 1034 GTCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1093
QY 887 TCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 946
Db 1094 TCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1153
QY 947 ACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1006
Db 1154 ACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1213

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QY 1007 TCTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1066
Db 1214 TCTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1273
QY 1067 CCAACATCTGAAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1126
Db 1274 CCAACATCTGAAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1333
QY 1127 ACAATGTCCGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1186
Db 1334 ACAATGTCCGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1393
QY 1187 ACCGCTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1246
Db 1394 ACCGCTTATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTC 1453
QY 1247 GCGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1306
Db 1454 GCGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1513
QY 1307 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1366
Db 1514 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1573
QY 1367 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1426
Db 1574 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1633
QY 1427 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1486
Db 1634 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1693
QY 1487 CATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1546
Db 1694 CATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1753
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Db 1754 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1813
QY 1607 GGGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1666
Db 1814 GGGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1873
QY 1667 CCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1726
Db 1874 CCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1933
QY 1727 CTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1786
Db 1934 CTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1993
QY 1787 CCTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1846
Db 1994 CCTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 2053
QY 1847 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1906
Db 2054 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 2113
QY 1907 CCTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1966
Db 2114 CCTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 2273
QY 1967 AGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 1980
Db 2174 AGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCG 2287

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RESULT 4
 US-09-761-640-1
 ; Sequence 1, Application US/09761640
 ; Patent No. US20020137042A1


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; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000964-CIP
; CURRENT APPLICATION NUMBER: US/09/761,640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2704
; TYPE: DNA
; ORGANISM: Human
US-09-761-640-1

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Query Match 89.6%; Score 1774; DB 10; Length 2704;

Best Local Similarity 95.1%; Pred. No. 0;

Matches 1882; Conservative 0; Mismatches 0; Indels 98; Gaps 1;

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QY 1 ATGGCCCTGTCAAGTGAAGCGTTGCCCCCGGAGAGCGGCGCTCCAGCCCGTGGG 60
DB 94 ATGACCTGTGTCAAGTGAAGCGTTGCCCCCGGAGAGCGGCGCTCCAGCCCGTGGG 153
QY 61 CCTGGGACCAAGCGGCTCCAGGAAAGAGTGAAGTCCAGCGAAGGAGAGCTTTGGG 120
DB 154 CCTGGGACCAAGCGGCTCCAGGAAAGAGTGAAGTCCAGCGAAGGAGAGCTTTGGG 213
QY 121 CTCCTGGGAGTGTCTCTGGAGTGCAGATGAGAGGAGCAATGATGATGAGAGAGCC 180
DB 214 CTCCTGGGAGTGTCTCTGGAGTGCAGATGAGAGGAGCAATGATGATGAGAGAGCC 273
QY 181 AATTTCAGACCAAGAGAAAGGCGCGAGTGAAGAGAGTCCAGGGGAGCAAGCAAGC 240
DB 274 AATTTCAGACCAAGAGAAAGGCGCGAGTGAAGAGAGTCCAGGGGAGCAAGCAAGC 333
QY 241 TTCGGGCAAGATCCAGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 300
DB 334 TTCGGGCAAGATCCAGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 393
QY 301 AAGGTACAGCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 360
DB 394 AAGGTACAGCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 453
QY 361 CGGCGTCCCGGCTCCGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 454 CGGCGTCCCGGCTCCGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 513
QY 421 CAGGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 514 CAGGATGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 573
QY 481 CTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 574 CTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 633
QY 541 TTCAGGTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 634 TTCAGGTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 693
QY 601 TGGGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 694 TGGGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 753
QY 661 CCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 754 CCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 813
QY 721 AGTGTCTTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 814 AGTGTCTTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
QY 781 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840

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DB 874 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 933
QY 841 AAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 934 AAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
QY 901 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB 994 GAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
QY 961 CTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 1054 CTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1113
QY 1021 GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1114 GAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1173
QY 1081 ATGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1174 ATGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
QY 1141 TGGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1234 TGGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293
QY 1201 GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1294 GCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
QY 1261 GCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1354 GCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1413
QY 1321 CGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1414 CGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1473
QY 1381 CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1474 CAGATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
QY 1441 GGTGGGCTTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1498 ----- 1497
QY 1501 CCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1498 --GCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1555
QY 1561 GCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1556 GCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
QY 1621 ATCAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1616 ATCAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675
QY 1681 GAGGTCTTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1676 GAGGTCTTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1735
QY 1741 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1736 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1795
QY 1801 CAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
DB 1796 CAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1855
QY 1861 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

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RESULT 5
US-09-761-640-7

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? Sequence 7, Application US/09761640
? Patent No. US20020137042A1
? GENERAL INFORMATION:
? APPLICANT: WEI, Ming-Hui et al
? TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS
? TITLE OF INVENTION: AND USES THEREOF
? FILE REFERENCE: CLO00964-CIP
? CURRENT APPLICATION NUMBER: US/09/761,640
? CURRENT FILING DATE: 2001-01-18
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 7
? LENGTH: 2704
? TYPE: DNA
? ORGANISM: Human
? US-09-761-640-7

```

| | | | | |
|----------------------------|-------|---------------|------------|--------------|
| Query Match | 89.6% | Score 1774; | DB 10; | Length 2704; |
| Best Local Similarity | 95.1% | Pred. No. 0; | | |
| Matches 1882; Conservative | 0; | Mismatches 0; | Indels 98; | Gaps 1 |

| | | |
|----|--|-----|
| Qy | ATGACCCTGGTACACATGAGCCGTTCCGCCCCCGGCGACGGCGCTCCACGCCCCTGGGG | 60 |
| Db | ATGACCCTGGTACACATGAGCCGTTCCGCCCCCGGCGACGGCGCTCCACGCCCCTGGGG | 153 |
| Qy | CCCTGGAGCCAGCGGCTCCAGCAAGAGTGCATCCAGCGAAGCAGAGCTTTGGCGTG | 120 |
| Db | CCCTGGAGCCAGCGGCTCCAGCGAAGAGTGCATCCAGCGAAGCAGAGCTTTGGCGTG | 213 |
| Qy | CTCCGGTGGGGCTGTCTCTGGGACTGCAGATGAGAGGGGCAATGATGATGAGCAGAGGCC | 180 |
| Db | CTCCGGTGGGGCTGTCTCTGGGACTGCAGATGAGAGGGGCAATGATGATGAGCAGAGGCC | 273 |
| Qy | AGTTCTGAGCCCAACAGAAAGGCCCGAGTGAAGAGAGCTCCACGGGAGCCAGACAGAC | 240 |
| Db | AGTTCTGAGCCCAACAGAAAGGCCCGAGTGAAGAGAGCTCCACGGGAGCCAGACAGAC | 333 |
| Qy | TTGGGGCAAGATCCACAGTCCCCAGAAAGAGAGAGAGAGAGAGCGCAGACTGCACCTC | 300 |
| Db | TTGGGGCAAGATCCACAGTCCCCAGAAAGAGAGAGAGAGAGAGCGCAGACTGCACCTC | 393 |
| Qy | ATGGTACAGCTGTGAGGCCCGAGGATACATCCGCCCTGGCAGCCACGCTGAGAGCACC | 360 |
| Db | ATGGTACAGCTGTGAGGCCCGAGGATACATCCGCCCTGGCAGCCACGCTGAGAGCACC | 453 |
| Qy | CGGCTTCCCCGGCTCCGCTACTCTGTGTGATTTCTACGAGAAAGAGAAAGTCTGAGC | 420 |
| Db | CGGCTTCCCCGGCTCCGCTACTCTGTGTGATTTCTACGAGAAAGAGAAAGTCTGAGC | 513 |
| Qy | CAGGATGAGACGGTCTCTCTGGGCGTGAATTTCCCTGACAGAGACTCCCCCACTCAGC | 480 |
| Db | CAGGATGAGACGGTCTCTCTGGGCGTGAATTTCCCTGACAGAGACTCCCCCACTCAGC | 573 |
| Qy | CTGGGCGTGTCTTGGCCCTCTGGAGTACACCCAGGTGTACTTGAATGAGACGGGGCC | 540 |
| Db | CTGGGCGTGTCTTGGCCCTCTGGAGTACACCCAGGTGTACTTGAATGAGACGGGGCC | 633 |
| Qy | TTGAGGCTACCGCTGGTGGGCAAGCGGAGATCTTCAAGCCCAATCTCATCCAGACATG | 600 |
| Db | TTGAGGCTACCGCTGGTGGGCAAGCGGAGATCTTCAAGCCCAATCTCATCCAGACATG | 693 |
| Qy | TGGGCAACCTCAGGATTTGCAACCAAGCATGTAGGAGAGCTTAGGCAAGGCGCTTGTGA | 660 |

| | | | |
|----|------|---|------|
| Dp | 654 | GGGGCACTCCAGGTATTGCAACCAAGCAATGTAGGACAGCTTAGAGGAGGCGCTTGTA | 753 |
| Qy | 661 | CCGGGTGGCACTAGTGCCTTCACCTTGGGCGACGCCACTACCAAGAGAGAACCTGAATCCCGAAG | 720 |
| Dp | 754 | CCGGGTGGCAATGTGCCCTTCACCTTGGGCGACGCCACTACCAAGAGAGAACCTGAATCCCGAAG | 813 |
| Qy | 721 | AGCTGCTCAATGAGTGGACGGCTATGAGCCGACCTGGAGTCTCTGCGGCGCTCCAGCGCC | 780 |
| Dp | 814 | AGCTGCTCAATGAGTGGAGGGCTATGAGCCGACCTGGAGTCTCTGCGGCGCTCCAGCGCC | 873 |
| Qy | 751 | GAGCCTGGCGGCTCCTCAGAACAGAGCAGATGAGACAGGCGATCCGTGCTGAGCTGG | 840 |
| Dp | 874 | GAGCCTGGCGGCTCCTCAGAACAGAGCAGATGAGACAGGCGATCCGTGCTGAGCTGG | 933 |
| Qy | 841 | AAAGCTTGAATGTCAGAGCCTTGAGAGTGTCACTTCAAAGAGATCCCGACGAGCTGTG | 900 |
| Dp | 934 | AAAGCTTGAATGTCAGAGCCTTGAGAGTGTCACTTCAAAGAGATCCCGACGAGCTGTG | 993 |
| Qy | 901 | GAGCTGCGCTGGGGGCTCCCTTCAGACGATACCTGATCTTCATCGAACACAGATGCTG | 960 |
| Dp | 994 | GAGCTGCGCTGGGGGCTCCCTTCAGACGATACCTGATCTTCATCGAACACAGATGCTG | 1053 |
| Qy | 961 | CTGCTGCTGAGACACCGGGAGCCGAGCCCTCCCGATCTTCCCGACCTTACCTGGAGTCA | 1020 |
| Dp | 1054 | CTGCTGCTGAGACACCGGGAGCCGAGCCCTCCCGATCTTCCCGACCTTACCTGGAGTCA | 1113 |
| Qy | 1021 | GAGTGAACGACGAGAAACCTGAGAGAGCTGACAGAGAAAGGTCACCAATCTTGAAC | 1080 |
| Dp | 1114 | GAGTGAACGACGAGAAACCTGAGAGAGCTGACAGAGAAAGGTCACCAATCTTGAAC | 1173 |
| Qy | 1081 | ATGGCCCGGGAGATTGACAACTTTACCTTACCGGCTTCAACCTTACCAATGTGGCGCTC | 1140 |
| Dp | 1174 | ATGGCCCGGGAGATTGACAACTTTACCTTACCGGCTTCAACCTTACCAATGTGGCGCTC | 1233 |
| Qy | 1141 | TGGGATGAGAGTGCAGCCAGCTCTCCGACCTGAGAGAGAGACGCAACCGCTTATGAG | 1200 |
| Dp | 1234 | TGGGATGAGAGTGCAGCCAGCTCTCCGACCTGAGAGAGAGAGCAACCGCTTATGAG | 1293 |
| Qy | 1201 | GCTGCAAGAGCAACAGGCGACCCACAGTGTGTCCATTGCAAGATGGCGCTACGCGCTCA | 1260 |
| Dp | 1294 | GCTGCAAGAGCAACAGGCGACCCACAGTGTGTCCATTGCAAGATGGCGCGTACGCGCTCA | 1353 |
| Qy | 1261 | GCGGCAAGAGCTCGGCGCTTATGCCATGAAGAGAACAAATGACCTGAGACAGGCGCTG | 1320 |
| Dp | 1354 | GCGGCAAGAGCTCGGCGCTTATGCCATGAAGAGAACAAATGACCTGAGACAGGCGCTG | 1413 |
| Qy | 1321 | CGCCACGTGACAGAGCTCCGGCCCATGCGCCCGCCCAACCTTGCTTCTTGCGCAGCTG | 1380 |
| Dp | 1414 | CGCCACGTGACAGAGCTCCGGCCCATGCGCCCGCCCAACCTTGCTTCTTGCGCAGCTG | 1473 |
| Qy | 1381 | CAGATCTTACAGGGGATCTTGAACGGCCAGCCGCGCAGAGCCATGTCTGGAGAGAGAAAGTG | 1440 |
| Dp | 1474 | CAGATCTTACAGGGGATCTTGAACGGCCAGCCGCGCAGAGCCATGTCTGGAGAGAGAAAGTG | 1497 |
| Qy | 1441 | GATGGGGTCTCCCAAGAGAGACCCAGACCCCTTGAATCTTACACCATTCGCCACTT | 1500 |
| Dp | 1498 | ----- | 1497 |
| Qy | 1501 | CCGCCAGAACTGAGGCTGTGGGAGAGAGAGTGTAGGCATGAAAGAGCCAGACCA | 1560 |
| Dp | 1498 | --GCCAGAACTGAGGCTGTGGGAGAGAGAGTGTGTAGGCATGAAAGAGCCAGACCA | 1555 |
| Qy | 1551 | GCCCCGAAAGAGAGGCTGGGGCCACGGCCACGTTAAACCTCCGAGGGGATCATGAGTTC | 1620 |
| Dp | 1556 | GCCCCGAAAGAGAGGCTGGGGCCACGGCCACGTTAAACCTCCGAGGGGATCATGAGTTC | 1615 |
| Qy | 1621 | ATCACTCTTCTGAGACCCCTCTTGGAGCTGAGAGCACTTCAGAGACCAAGTGAATGCA | 1680 |
| Dp | 1616 | ATCACTCTTCTGAGACCCCTCTTGGAGCTGAGAGCACTTCAGAGACCAAGTGAATGCA | 1675 |
| Qy | 1681 | GAGGTCTTCTTCCCAAGAGTCTTTCACATGAAGAGCTTCGACGCCCTTCCACAGCTT | 1740 |
| Dp | 1735 | GAGGTCTTCTTCCCAAGAGTCTTTCACATGAAGAGCTTCGACGCCCTTCCACAGCTT | 1735 |

| Accession | Sequence | Position |
|-----------|--|----------|
| QY | 1741 GCAAGGACCAAGAGGAGGCGACAGAGTGGACAGAGGGGGCTTACAGCTGGCCCTTAAGTCCCG | 1800 |
| Db | 1736 GCAAGGACCAAGAGGAGGCGACAGAGTGGACAGAGGGGGCTTACAGCTGGCCCTTAAGTCCCG | 1795 |
| QY | 1801 CAGTCAGTGGTTACCTCCCTCAGGGCAGTGCCTGTGTGGCAACCGGACCCAGAGCCTTCCAG | 1860 |
| Db | 1796 CAGTCAGTGGTTACCTCCCTCAGGGCAGTGCCTGTGTGGCAACCGGACCCAGAGCCTTCCAG | 1855 |
| QY | 1861 GAGCAGGACGACGAGGGCAGGGGCGAGGGGCGAAGGGAGGCTTCATTCTCTAAGCCCAAG | 1920 |
| Db | 1856 GAGCAGGACGACGAGGGCAGGGGCGAGGGGCGAAGGGAGGCTTCATTCTCTAAGCCCAAG | 1915 |
| QY | 1921 TTCCGGGAAGGTGTAGACAGGCCACGGCTGCAATGACATGAGAGAGGAGGAGGCGCTGAC | 1980 |
| Db | 1916 TTCCGGGAAGGTGTAGACAGGCCACGGCTGCAATGACATGAGAGAGGAGGAGGCGCTGAC | 1975 |

RESULT 6
US-10-363-676-10

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1 TITLE OF INVENTION: REGULATION OF HUMAN MAP KINASE PHOSPHATASE-LIKE ENZYME
2
3 FILE REFERENCE: LIO122 Foreign Countries
4
5 CURRENT APPLICATION NUMBER: US/10/363,676
6
7 CURRENT FILING DATE: 2003-03-06
8
9 PRIOR APPLICATION NUMBER: US 60/230,709
10
11 PRIOR FILING DATE: 2000-09-07
12
13 NUMBER OF SEQ ID NOS: 11
14
15 SOFTWARE: PatentIn version 3.1

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ORGANISM: Homo sapiens
US-10-363-676-10

| Query Match | 85.1% | Score 1684 | DB 13 | Length 2332 |
|-----------------------|--|-------------|---------------|-------------|
| Best Local Similarity | 95.0% | Pred. No. 0 | | |
| Matches 1852 | Conservative | 0 | Mismatches 75 | Indels 23 |
| | | | Gaps | 10 |
| QY | CGGGCGCTCCACGCGCCCGTGGGGCCCTGGAGCCAGCGGTCCAGCGCAAGTGCATCTCA | 98 | | |
| Db | CGCCCTCACCTCGGGGCTGTCTCTTCGGCAGACCTGTGTCCAGCGAAGATCGACTCCA | 206 | | |
| QY | CGGAAAGGAGAGACTTTGGGTGCTCC-CTGGGGCTGCTCTCTGGAACTGAGAGATGAGAGGG | 157 | | |
| Db | CGGA---AGAGCTTTGCGTGTCTCTGTGGGCGTCTCTGAGATGAGAGATGAGAGGG | 262 | | |
| QY | ACAATGATGATGACAGCAGAGGCCAATTGTGAGCCACAGAGAAGGCCCGAGTGGAGAG | 217 | | |
| Db | ACATGATGATGACAGCAGAGGCCAGTGTGTGAGCCACAGAGAAGGCCCGAGTGGAGAG | 322 | | |
| QY | AGCTCCAGGGG---ACCAACACACTT--CGGGAAAGATCCCAAGATCCCCCAAGACA | 272 | | |
| Db | AGCTCCAGGGGAAACCAAGACACTTGTGATGAAAGATCCCAAGATCCCCCAAGACA | 382 | | |
| QY | GGAGAGCAGAGGAGACCTGCACCTCATGTACAGCTGCTGTGAGGCGCAGAGATGACAT | 332 | | |
| Db | GGAGAGCAGAGGAGCAGCACTGCACCTCATGAGGCGTGTGAGGCCCGCAGAGATGACAT | 442 | | |
| QY | CGCGCTGGCA--GCTCACTGGAAGGACCCCGGCTCTCCCGGCTTCGTTACTCTG---- | 385 | | |
| Db | CGACTTGAAGCCCAAGCTGAAGGACCCCGGCTCTCCCGGATTCGATTAACCTTGCT | 502 | | |
| QY | TGTAGTATTCTACACGAGAA--GAGAGAGTGTGAG--CCAGATGAGACGATCTCTGGG | 443 | | |
| Db | TGTAGTATTCTACACGAGAGGAGAAAGTGTGAGCCCAAGATGAGACGATCTCTGGG | 562 | | |
| QY | CTGAGATTTCCCTGACAGCAAGCTTCCCAAGTGAACCTTGAGGCTTGATCTTGCCCTCT | 502 | | |
| Db | ACGTGATTTCCCTGACAGCAAGCTTCCCAAGTGAACCTTGAGGCTTGATCTTGCCCTCT | 622 | | |

| | | | |
|----|------|---|------|
| OY | 503 | GGAGTGAACCCAGAGTGAATTAATGAGACGGGGGCTTCAGAGTACGCTCTGTGTGGG | 566 |
| Db | 623 | GGAGTGAACCCAGAGTGAATTAATGAGACGGGGGCTTCAGAGTACGCTCTGTGTGGG | 682 |
| OY | 563 | AAAGCCGAGTCTTCAAGCCCATCTCCATCCAGACCAATGTGGGCGCACTCCAGGTATTGC | 622 |
| Db | 683 | AAAGCCGAGTCTTCAAGCCCATCTCCATCCAGACCAATGTGGGCGCACTCCAGGTATTGC | 742 |
| OY | 623 | ACCAGAGATGTGAGGAGCTCTAGCGACGGGCTTTGTACCGGGTGGAGATGCTCCACT | 682 |
| Db | 743 | ACCAGAGATGTGAGGAGCTCTAGCGACGGGCTTTGTACCGGGTGGAGATGCTCCACT | 802 |
| OY | 683 | GGGCCAGCCACTACCGAGAGACTGAATCTCGAACAGAGTTGCTCAATGATGAGACGG | 742 |
| Db | 803 | GGGCCAGCCACTACCGAGAGACTGAATCTCGAACAGAGTTGCTCAATGATGAGACGG | 862 |
| OY | 743 | CTATGGCCGACCTGAGAGCTCTGTGGGCTCCCAAGCCGAGACCTGGGGGCTCCAGAAC | 802 |
| Db | 863 | CTATGGCCGACCTGAGAGCTCTGTGGGCTCCCAAGCCGAGACCTGGGGGCTCCAGAAC | 922 |
| OY | 803 | AGGAGCAGATGAGACGAGCGATCCGTGCTGAAGCTGTGAAAATGTTGAGATGCACTGAC | 862 |
| Db | 923 | AGGAGCAGATGAGACGAGCGATCCGTGCTGAAGCTGTGAAAATGTTGAGATGCACTGAC | 982 |
| OY | 863 | TGAGAGAGTCACTTCCAAAGATTCGACAGGCTCTGAGAGTCTCGGCTGGAGCTCCGCC | 922 |
| Db | 983 | TGAGAGAGTCACTTCCAAAGATTCGACAGGCTCTGAGAGTCTCGGCTGGAGCTCCGCC | 1042 |
| OY | 923 | TTCAGCAGTACCGTGACTTTCATGCAACAACAGATGCTGCTGTGTGGCACAGCGGAGCC | 982 |
| Db | 1043 | TTCAGCAGTACCGTGACTTTCATGCAACAACAGATGCTGCTGTGTGGCACAGCGGAGCC | 1102 |
| OY | 983 | GAGGCTCCCGCATTTCCGCCCACTCTACCTGAGGCTCAGAGTGGAAAGCAACAACCTGG | 1042 |
| Db | 1103 | GAGGCTCCCGCATTTCCGCCCACTCTACCTGAGGCTCAGAGTGGAAAGCAACAACCTGG | 1162 |
| OY | 1043 | AGGAGCTGACAGAGAAAGGGTCAACCAATCTTGAACATGTGCCCGGAGATTGACAAT | 1102 |
| Db | 1163 | AGGAGCTGACAGAGAAAGGGTCAACCAATCTTGAACATGTGCCCGGAGATTGACAAT | 1219 |
| OY | 1103 | TCTACCTGAGCGCTTCACTCACTACCAATGTGCGCTCTGGAGTGAAGAGCGGCCAGC | 1162 |
| Db | 1220 | TCTACCTGAGCGCTTCACTCACTACCAATGTGCGCTCTGGAGTGAAGAGCGGCCAGC | 1279 |
| OY | 1163 | TGCTGCGGCACTGGAAGAGACGACCGCTTCAATTGAGGCTGCAAGACACAGGGCACCC | 1222 |
| Db | 1280 | TGCTGCGGCACTGGAAGAGACGACCGCTTCAATTGAGGCTGCAAGACACAGGGCACCC | 1339 |
| OY | 1223 | ACGTGCTGTGATCACTGCAAGATGTGGGCTCAAGCCCTCAGCGGCGCACAGTGTGGCTATG | 1282 |
| Db | 1340 | ACGTGCTGTGATCACTGCAAGATGTGGGCTCAAGCCCTCAGCGGCGCACAGTGTGGCTATG | 1399 |
| OY | 1283 | CCATGAAGACGATACGATTCAGGCTTGAGACAGGCTCTGCGCCACAGTGCAGAGCTCCGGC | 1342 |
| Db | 1400 | CCATGAAGACGATACGATTCAGGCTTGAGACAGGCTCTGCGCCACAGTGCAGAGCTCCGGC | 1459 |
| OY | 1343 | CCATGCGCGCGCCCAACCTGTGCTTCTGTGGCGCAGCTGACGATTTACACAGGCACTCTGA | 1402 |
| Db | 1460 | CCATGCGCGCGCCCAACCTGTGCTTCTGTGGCGCAGCTGACGATTTACACAGGCACTCTGA | 1519 |
| OY | 1403 | CGGCGCAGCCGCGCAAGCCATGTCTGTGGAGCAAAAGTGGGTGGGGTCTCCCAAGAGAGC | 1462 |
| Db | 1520 | CGGCGCAGCCGCGCAAGCCATGTCTGTGGAGCAAAAGTGGGTGGGGTCTCCCAAGAGAGC | 1579 |
| OY | 1463 | ACCAGGCCCCGAAAGTCTCTACACCATTTCCACCTCTTCCGCGCAAACTTGAGGGTGTG | 1522 |
| Db | 1580 | ACCAGGCCCCGAAAGTCTCTACACCATTTCCACCTCTTCCGCGCAAACTTGAGGGTGTG | 1639 |
| OY | 1523 | GGGAGGAGAAAGTTGTAGGCAATGGAAGAAGACAGGAGCCCGGAAGAGAGGCTGTGGC | 1582 |
| Db | 1640 | GGGAGGAGAAAGTTGTAGGCAATGGAAGAAGACAGGAGCCCGGAAGAGAGGCTGTGGC | 1699 |

| | | | |
|----|------|---|------|
| QY | 1583 | AAGGCGCAACGATATAAAGCTCCGAGAGGGGATAGAGGTCATCAAGTCTTCTTGAGCGCTCT | 1642 |
| Db | 1700 | CACGCGCAACGATATAAAGCTCCGAGAGGGGATCAATGAGTCCAATAGCTTTCTGAGCGCTCT | 1759 |
| QY | 1643 | TGAGAGCTGAGAGCACTTCAGAGACCAAGTGAATGCCAAGGTCCTTCCTTCCACGAGT | 1702 |
| Db | 1760 | TGAGAGCTGAGAGCACTTCAGAGACCAAGTGAATGCCAAGGTCCTTCCTTCCACGAGT | 1819 |
| QY | 1703 | CTTCACATGAAGAGCCTCTGCAGCCCTTCCACAGCTTGCAGAAGACCAAGGAGGCCAGC | 1763 |
| Db | 1820 | CTTCACATGAAGAGCCTCTGCAGCCCTTCCACAGCTTGCAGAAGACCAAGGAGGCCAGC | 1879 |
| QY | 1763 | AGGTGGAACAGGAGGGGCTCAGGCTGGCCCTGAAGTCCCGCAGTCAAGTGTATACCTCCACAG | 1822 |
| Db | 1880 | AGGTGGAACAGGAGGGGCTCAGGCTGGCCCTGAAGTCCCGCAGTCAAGTGTATACCTCCACAG | 1939 |
| QY | 1823 | GCAGTGCCTGTGTGGCCCAACCGGACCCAGGCTTTCAGAGACAGGAGCAGGCGCAGGCGC | 1882 |
| Db | 1940 | GCAGTGCCTGTGTGGCCCAACCGGACCCAGGCTTTCAGAGAGGAGAGCAGGCGCAGGCGC | 1999 |
| QY | 1883 | AGGAGCAGAGGAGAGCCCTGCATTTCTTACGCCCTCAAGTTCGGAAAGTGGTGAACAGG | 1943 |
| Db | 2000 | AGGAGCAGAGGAGAGCCCTGCATTTCTTACGCCCTCAAGTTCGGAAAGTGGTGAACAGG | 2055 |
| QY | 1943 | CCAGCGTCATGACAGGTGAGAGAGGAGCGG | 1972 |
| Db | 2060 | CCAGCGTCATGACAGGTGAGAGAGGAGCGG | 2089 |

```

RESULT 7
US-09-955-732-20
Sequence 20, Application US/09955732
Publication No. US2002018223A1
GENERAL INFORMATION:
APPLICANT: Lucne, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ. ID NOS: 27
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ. ID NO 20
LENGTH: 1416
TIPE: DNA
ORGANISM: Mus musculus
US-09-955-732-20

```

| | | | | |
|-----------------------|-----------------|---------------|-----------|--------------|
| Query Match | 71.2% | Score 1409; | DB 10; | Length 1416; |
| Best Local Similarity | 100.0% | Pred. No. 0; | | |
| Matches 1409; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | | | | |
|----|-----|----------------|---------------------------|---------------------|------------|-----|
| Qy | 1 | ATGGCCCTGGTCA | CAGTAGACCGCTTGCC | CCCCGGGCAAGCGCGCTCA | GCCCTTGAGG | 60 |
| | | | | | | |
| Db | 1 | ATGGCCCTGGTCA | CAETGAGCCGCTTCC | CCCCGGGCAAGCGCGCTCA | GCCCTTGAGG | 60 |
| Qy | 61 | CCCTGGGAC | CAGCGGCTCCAGCGAAGAGTCA | CTCAAGCGAAGCAGAC | CTTTCGGTG | 120 |
| Db | 61 | CCCTGGGAC | CAGCGCGGCTCCAGCGAAGAGTCA | CTCAAGCGAAGCAGAC | CTTTCGGTG | 120 |
| Qy | 121 | CTCCGTGGGCG | CTGCTCTGGGACTGAGAGATG | AGGGGCAATGATATG | CAGCAGAGGC | 180 |
| Db | 121 | CTCCGTGGGCG | CTGCTCTGGGACTGAGAGATG | AGGGGCAATGATATG | CAGCAGAGGC | 180 |
| Qy | 181 | AGTTCTGAGCA | CAGAGAGGCCCCCGAGTAGAGAGAG | CTCCACGGGAC | CAGACAGAC | 240 |
| Db | 181 | AGTTCTGAGCA | CAGAGAGGCCCCCGAGTAGAGAGAG | CTCCACGGGAC | CAGACAGAC | 240 |
| Qy | 241 | TTGGGGCAAGAGAT | CCCCAGATCCCGAAGACAGAGAGAG | CAGAGGCAGAC | CTTCGACCTC | 300 |
| Db | 241 | TTGGGGCAAGAGAT | CCCCAGATCCCGAAGAGAGAGAG | CAGAGGCAGAC | CTTCGACCTC | 300 |
| Qy | 301 | ATGAGTACAGT | GTGTGAGCCCGAGAGATATC | CGCTTGACGCCAC | CTGTGAGGAC | 360 |

| | | | |
|----|------|---|------|
| Db | 301 | ATGCTACAGCTGCTGAGGCGCGAGATGACATCCGGCTGGCACCCAGCTGGAGGACCC | 360 |
| Qy | 361 | CGGCTCTCCCGGCGCTCCGCTACCTGACGTGATGTTCTTACAAGAAAGAGAGATCTGAGC | 420 |
| Db | 361 | CGGCTCTCCCGGCTCTCCGCTACCTGACGTGATGTTCTTACAAGAAAGAGAGATCTGAGC | 420 |
| Qy | 421 | CAGATGAGACGGTCTCTCTGGGCGTGGATTTTCCCTGACAGCAGCTTCCCACTGCACC | 480 |
| Db | 421 | CAGATGAGACGGTCTCTCTGGGCGTGGATTTTCCCTGACAGCAGCTTCCCACTGCACC | 480 |
| Qy | 481 | CTGGGCGCTGGTCTTGGCCCTCTGGAGTGAACACCAGGTGTACTTAGTGGAGA | 540 |
| Db | 481 | CTGGGCGCTGGTCTTGGCCCTCTGGAGTGAACACCAGGTGTACTTAGTGGAGA | 540 |
| Qy | 541 | TTACGCTGACGTGTGTGGGCAAAAGCCGATCTTCAAGCCCATTTCCATCCAGACATG | 600 |
| Db | 541 | TTACGCTGACGTGTGTGGGCAAAAGCCGATCTTCAAGCCCATTTCCATCCAGACATG | 600 |
| Qy | 601 | TGGGCGCACACTCCAGGATTTGACACAAGCATGTGAGGCACTGTAGCAGCGGCTTGTGA | 660 |
| Db | 601 | TGGGCGCACACTCCAGGATTTGACACAAGCATGTGAGGCACTGTAGGCAAGCGGCTTGTGA | 660 |
| Qy | 661 | CCGGGTGGCAGTGCCTCTCACTTGGGCGCAGCTTACCGCACAAGAGATCTGGAACAG | 720 |
| Db | 661 | CCGGGTGGCAGTGCCTCTCACTTGGGCGCAGCTTACCGCACAAGAGATCTGGAACAG | 720 |
| Qy | 721 | AGCTGCTCATATGAGTGGAGCGGCTATGGCCGACCTGGAGTCTGTGCGGCTCCAGCGCC | 780 |
| Db | 721 | AGCTGCTCATATGAGTGGAGCGGCTATGGCCGACCTGGAGTCTGTGCGGCTCCAGCGCC | 780 |
| Qy | 781 | GAGCTTGGCGGGTCTCTACAACAGAGACATAGAGAGAGGCGATCCGTGCTGAGCTGG | 840 |
| Db | 781 | GAGCTTGGCGGGTCTCTACAACAGAGACATAGAGAGAGGCGATCCGTGCTGAGCTGG | 840 |
| Qy | 841 | AAATGTTTGATGTCACTGACCTGGAGAGTGCATCTTCCAAAGATCCCGCAGGCTCTG | 900 |
| Db | 841 | AAATGTTTGATGTCACTGACCTGGAGAGTGCATCTTCCAAAGATCCCGCAGGCTCTG | 900 |
| Qy | 901 | GAGCTGCGCTCGGGGCTTCCCTCTCAGCAGTACCGGTACTTTCATGCAACACAGATGCTG | 960 |
| Db | 901 | GAGCTGCGCTCGGGGCTTCCCTCTCAGCAGTACCGGTACTTTCATGCAACACAGATGCTG | 960 |
| Qy | 961 | CTGCTGGTGGCACAAGCGGAGCCAGAGCTCCCGCATTTTCCCCCACTTACCTTGGCTCA | 1020 |
| Db | 961 | CTGCTGGTGGCACAAGCGGAGCCAGAGCTCCCGCATTTTCCCCCACTTACCTTGGCTCA | 1020 |
| Qy | 1021 | GAGTGAACCGACGAAACCTGAGAGAGCTGCAAGGAAACAGGGTCAACCCATTTTAAAC | 1080 |
| Db | 1021 | GAGTGAACCGACGAAACCTGAGAGAGCTGCAAGGAAACAGGGTCAACCCATTTTAAAC | 1080 |
| Qy | 1081 | ATGGCCCGGGAGATTGACAACTTTACCTTGAGGCGCTTCACTTACCAATATGTCGCTC | 1140 |
| Db | 1081 | ATGGCCCGGGAGATTGACAACTTTACCTTGAGGCGCTTCACTTACCAATATGTCGCTC | 1140 |
| Qy | 1141 | TGGATGAGAGTGGGCCCAGCTCTGCGGACTGGAAGAGAGACCCGCTTCAATTAGAG | 1200 |
| Db | 1141 | TGGATGAGAGTGGGCCCAGCTCTGCGGACTGGAAGAGAGACCCGCTTCAATTAGAG | 1200 |
| Qy | 1201 | GCTCAAGAGACAGGAGCAACCAAGTGTGTCACTGCAAGATGGGCGTCAAGCGCTCA | 1260 |
| Db | 1201 | GCTCAAGAGACAGGAGCAACCAAGTGTGTCACTGCAAGATGGGCGTCAAGCGCTCA | 1260 |
| Qy | 1261 | GCGGCGCAGTGTGGCTTATGCCATTAAGCATGACATGCAATGCAACCTGGAGAGGCGCTG | 1320 |
| Db | 1261 | GCGGCGCAGTGTGGCTTATGCCATTAAGCATGACATGCAATGCAACCTGGAGAGGCGCTG | 1320 |
| Qy | 1321 | CGGCAAGTGAAGAGCTCCGGCCCATGCGCGCCCAACCTGGCTTCTGTCGCGCAGCTG | 1380 |
| Db | 1321 | CGGCAAGTGAAGAGCTCCGGCCCATGCGCGCCCAACCTGGCTTCTGTCGCGCAGCTG | 1380 |
| Qy | 1381 | CAGATTCACAGGCAATCTGACGGCCAG | 1409 |


```

1      RESULT 9
2      US-09-814-353-19925
3      ; Sequence 19925, Application US/09814353
4      ; Publication NO. US20030165831A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Lee, John
7      ; APPLICANT: Thompson, Pamela
8      ; APPLICANT: Lillie, James
9      ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
10     ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
11     ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
12     ; FILE REFERENCE: MRI-006B
13     ; CURRENT APPLICATION NUMBER: US/09/814,353
14     ; CURRENT FILING DATE: 2001-03-21
15     ; PRIOR APPLICATION NUMBER: US 60/191,031
16     ; PRIOR FILING DATE: 2000-03-21
17     ; PRIOR APPLICATION NUMBER: US 60/207,124
18     ; PRIOR FILING DATE: 2000-05-25
19     ; PRIOR APPLICATION NUMBER: US 60/211,940
20     ; PRIOR FILING DATE: 2000-06-15
21     ; PRIOR APPLICATION NUMBER: US 60/216,820
22     ; PRIOR FILING DATE: 2000-07-07
23     ; PRIOR APPLICATION NUMBER: US 60/220,661
24     ; PRIOR FILING DATE: 2000-07-25
25     ; PRIOR APPLICATION NUMBER: US 60/257,672
26     ; PRIOR FILING DATE: 2000-12-21
27     ; NUMBER OF SEQ ID NOS: 22037
28     ; SOFTWARE: FastSeq for Windows Version 4.0
29     ; SEQ ID NO 19925
30     ; LENGTH: 2083
31     ; TYPE: DNA
32

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| | | | | | | | |
|----------------------------|-------|------------|--------------|--------|----|--------|------|
| Query Match | 56.6% | Score | 1121.4 | DB | 13 | Length | 2083 |
| Best Local Similarity | 95.3% | Pred | No. 3.8e-283 | | | | |
| Matches 1146; Conservative | 0 | Mismatches | 56 | Indels | 0 | Gaps | 0 |

| | | | |
|----|-----|---|-----|
| QY | 775 | AGCGCCGAGCCTCGCGGGGCTCTCCAGAAACAGAGCGAGATGGAAACAGACGCGATCTCGTCTAG | 834 |
| Db | 74 | AGGGGCTCTGCTCCCGAGGCTCTCCAGAACAGAGACGAGATGGAAACAGACGCGATCTCGTCTAG | 133 |
| QY | 835 | CTGTGGAAGAGTTTGATGATCTCAGTACCTCGAGAGATGTCACTTCCAAAGAGATCCGCCAG | 894 |
| Db | 134 | CTGTGGAAGAGTTTGATGATCTCAGTACCTCGAGAGATGTCACTTCCAAAGAGATCCGCCAG | 193 |
| QY | 895 | GCTCTGAGAGCTGCGGCTCGGGGCTCCCGCTCCAGCGAGTACCGAGATTATTCAGCAACACAG | 954 |

| | | | |
|----|------|---|------|
| D | 194 | GCCTGTGAGGTGGCCCTGGGGGCTCCGCCCTCAGACAGAACCGTAGCTTCAATGCACCAACAG | 253 |
| OY | 955 | ATGCTGTCTGTGGTGGCACAAGCGGAGACCAAGGCTTCCCGCATTTTCCCGCACTCTACCTG | 1014 |
| D | 254 | ATGCTGTCTGTGGTGGCACAAGCGGAGACCAAGGCTTCCCGCATTTTCCCGCACTCTACCTG | 313 |
| OY | 1015 | GGCTCAGAGTGGAAACGACAGCAAACTCTGAGAGACTGTGAGAGAAAGAGGTCAACCAATC | 1074 |
| D | 314 | GGCTCAGAGTGGAAACGACAGCAAACTCTGAGAGACTGTGAGAGAAAGAGGTCAACCAATC | 373 |
| OY | 1075 | TTGAAACATGGCCCGGGAGATTGAACAATTACCTTGAGGGCTTCACTTACCAATGTG | 1134 |
| D | 374 | TTGAAACATGGCCCGGGAGATTGAACAATTACCTTGAGGGCTTCACTTACCAATGTG | 433 |
| OY | 1135 | CGGCTCTGGGATGAGAGTGGGCGCCAGCTGCTCCGCACTGGAAGAGAGCGCACCGCTTC | 1194 |
| D | 434 | CGGCTCTGGGATGAGAGTGGGCGCCAGCTGCTCCGCACTGGAAGAGAGCGCACCGCTTC | 493 |
| OY | 1195 | ATTGAGGCTGCAAGAGCACAAGGGCACTCCAGTCTGTGTCATCTGCAAGATGGGCTACG | 1254 |
| D | 494 | ATTGAGGCTGCAAGAGCACAAGGGCACTCCAGTCTGTGTCATCTGCAAGATGGGCTACG | 553 |
| OY | 1255 | CGCTCAGCGGCAACAGTGTGGGCTTATGGCATGAGACAGTACCAATGACCTGAGACAG | 1314 |
| D | 554 | CGCTCAGCGGCAACAGTGTGGGCTTATGGCATGAGACAGTACCAATGACCTGAGACAG | 613 |
| OY | 1315 | GCCTGTGGCACAAGTGCAGAGACTCCGGCCCATCGCCGCCCAACCTGTGCTTCTGCGC | 1374 |
| D | 614 | GCCTGTGGCACAAGTGCAGAGACTCCGGCCCATCGCCGCCCAACCTGTGCTTCTGCGC | 673 |
| OY | 1375 | CAGCTGACAGTCTTACAGGAGCATCTGACGGGCCACCGCCAGAGGCATGTCTGAGACAG | 1434 |
| D | 674 | CAGCTGACAGTCTTACAGGAGCATCTGACGGGCCACCGCCAGAGGCATGTCTGAGACAG | 733 |
| OY | 1435 | AAAGTGGGTGGGCTCTCCCGACAGAGACCCCAAGCTCTGAACTCTTACCACTTCCCA | 1494 |
| D | 734 | AAAGTGGGTGGGCTCTCCCGACAGAGACCCCAAGCTCTGAACTCTTACCACTTCCCA | 793 |
| OY | 1495 | CTCTTTCGCGCAGAACTTGAGGGTGTGGGGAGAGAAAGTTGTAGGCATGGAAGAGAC | 1554 |
| D | 794 | CTCTTTCGCGCAGAACTTGAGGGTGTGGGGAGAGAAAGTTGTAGGCATGGAAGAGAC | 853 |
| OY | 1555 | CAGGCAACCCCGAAGAAAGAGCTGGGCGCAAGGCCACGTATAAACCTCCAGGGGTCATG | 1614 |
| D | 854 | CAGGCAACCCCGAAGAAAGAGCTGGGCGCAAGGCCACGTATAAACCTCCAGGGGTCATG | 913 |
| OY | 1615 | AGGTCCATCAAGTCTTCTGAGACCTCTCTGAGCTGAGAGCACTCAAGAACCACTGAC | 1674 |
| D | 914 | AGGTCCATCAAGTCTTCTGAGACCTCTCTGAGCTGAGAGCACTCAAGAACCACTGAC | 973 |
| OY | 1675 | ATGCAAGAGTCTTCTTCCCAACGAATCTTACATGAAGAGCTCTGACAGCCCTTCCCA | 1734 |
| D | 974 | ATGCAAGAGTCTTCTTCCCAACGAATCTTACATGAAGAGCTCTTCTGACAGCCCTTCCCA | 1033 |
| OY | 1735 | CAGCTTCAAGAGCAAGAGAGAGCCACAGAGTGAACAAGGGGCTCTAGCTTCCCTGAAG | 1794 |
| D | 1034 | CAGCTTCAAGAGCAAGAGAGAGCCACAGAGTGAACAAGGGGCTCTAGCTTCCCTGAAG | 1093 |
| OY | 1795 | TCCCGCACAATGATGGTTAACCTTCAAGGCAATGTCCTGTGTGGTCAACCGAACCAAGCC | 1854 |
| D | 1094 | TCCCGCACAATGATGGTTAACCTTCAAGGCAATGTCCTGTGTGGTCAACCGAACCAAGCC | 1153 |
| OY | 1855 | TTCCAGAGAGCAGAGAGAGGGGACAGGGGACAGGGAGAGAGCCCTGATCTTCTTAAG | 1914 |
| D | 1154 | CAGGCGCACAAGAGAGAGTGGGGGCTGTGGAGAGGAGAGCCCTGTCAATTTACAGTGG | 1213 |
| OY | 1915 | CCAGAGTTCCGGAAGTGTGTGAGACACAGCCACGGTGCATGACATGAGAGAGAGGGGAG | 1974 |
| D | 1214 | ANAGAGAGCGGAAGTGTGNNNTTCAAGCANNGCCNACANAGCANNTTGAGAGAGAGGGGAG | 1273 |
| OY | 1975 | GC 1976 | |
| D | 1274 | GC 1275 | |

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RESULT 10
US-10-363-676-4
; Sequence 4, Application US/10363676
; Publication No. US20030170856A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN MAP KINASE PHOSPHATASE-LIKE ENZYME
; FILE REFERENCE: L10122 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/363,676
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/230,709
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-363-676-4

Query Match
Best Local Similarity 35.1%; Score 694; DB 13; Length 1755;
Matches 802; Conservative 0; Mismatches 0; Indels 98; Gaps 1;

QY 1081 ATGGCCCGGAGATTGACAACTTTACCTGAGCGCTTCACTTACCAATGTGCGCTC 1140
DB 322 ATGGCCCGGAGATTGACAACTTTACCTGAGCGCTTCACTTACCAATGTGCGCTC 381
QY 1141 TGGGATGAGAGATCGGCGCAGCTGCTGCGCAGTGGAGAGAGAGAGAGAGAGAGAG 1200
DB 382 TGGGATGAGAGATCGGCGCAGCTGCTGCGCAGTGGAGAGAGAGAGAGAGAGAGAG 441
QY 1201 GCTGCAAGAGACAGAGGAGACCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 442 GCTGCAAGAGACAGAGGAGACCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501
QY 1261 GGGGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 502 GGGGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
QY 1321 CGCCAGTGCAGAGAGCTCCGCGCCATTCGCGCCGCCAACCCTTGCTTCTGCGCCAGT 1380
DB 562 CGCCAGTGCAGAGAGCTCCGCGCCATTCGCGCCGCCAACCCTTGCTTCTGCGCCAGT 621
QY 1381 CAGATCTTACAGAGGAGCTTCTGACGGCCAGCGCCAGAGCCATGTCTGGAGAGAGAA 1440
DB 622 CAGATCTTACAGAGGAGCTTCTGACGGCCAGCGCCAGAGCCATGTCTGGAGAGAGAA 645
QY 1441 GATGGGGTCTCCCAAGAGAGAGACCCAGCGCTGAAAGTCTTACACATTTCCACCTTT 1500
DB 646 ----- 645
QY 1501 CCGCCAGAACTGAGGGTGTGTGGAGAGAGAAAGTTTGTAGAGCATGAAAGAGAGCCAG 1560
DB 646 --GCCAGAACTGAGGGTGTGTGGAGAGAGAAAGTTTGTAGAGCATGAAAGAGAGCCAG 703
QY 1561 GCGCCGAAAGAGAGAGCTGAGGCGCAGGCGCAGTAAACCTCCGAGGGGTGATAGAGTCC 1620
DB 704 GCGCCGAAAGAGAGAGCTGAGGCGCAGGCGCAGTAAACCTCCGAGGGGTGATAGAGTCC 763
QY 1621 ATCAGTCTTCTGAGAGCCCTCTTGGAGCTGAGAGACACCTCAGAGACAGAGTACATGCA 1680
DB 764 ATCAGTCTTCTGAGAGCCCTCTTGGAGCTGAGAGACACCTCAGAGACAGAGTACATGCA 823
QY 1681 GAGGCTTCTTCTTCCCAAGAGTCTTCACTGAAGAGCTTGTGAGACCTTCCCAAGT 1740
DB 824 GAGGCTTCTTCTTCCCAAGAGTCTTCACTGAAGAGCTTGTGAGACCTTCCCAAGT 883
QY 1741 GAAAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 884 GAAAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 943
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RESULT 11
US-10-363-676-8
; Sequence 8, Application US/10363676
; Publication No. US20030170856A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN MAP KINASE PHOSPHATASE-LIKE ENZYME
; FILE REFERENCE: L10122 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/363,676
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/230,709
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-363-676-8

Query Match
Best Local Similarity 24.8%; Score 491; DB 13; Length 599;
Matches 599; Conservative 0; Mismatches 0; Indels 98; Gaps 1;

QY 1024 TGGAGCGACCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
DB 1 TGGAGCGACCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 1084 GCCCGAGAGATTGACAACTTCTACCTGAGCGCTTCACTTACCAATGTGCGCTTGG 1143
DB 61 GCCCGAGAGATTGACAACTTCTACCTGAGCGCTTCACTTACCAATGTGCGCTTGG 120
QY 1144 GATGAGAGTGGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
DB 121 GATGAGAGTGGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 1204 GCAAGAGCAGAGGAGACCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
DB 181 GCAAGAGCAGAGGAGACCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 1264 GCGACAGTGTGCGCTTATGCTATGAAGAGAGTACGAATGACAGCTTGAAGAGAGAG 1323
DB 241 GCGACAGTGTGCGCTTATGCTATGAAGAGAGTACGAATGACAGCTTGAAGAGAGAG 300
QY 1324 CAGTGGAGAGAGTCCGCGCCATTCGCGCCGCCAACCCTTGCTTCTGCGCGCAGTGCAG 1383
DB 301 CAGTGGAGAGAGTCCGCGCCATTCGCGCCGCCAACCCTTGCTTCTGCGCGCAGTGCAG 360
QY 1384 ATTCACAGGAGCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
DB 361 ATTCACAGGAGCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
QY 1444 GGGGTCTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1503
DB 382 -----G 382
QY 1504 CCAAGACTGAGAGTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1563
DB 383 CCAAGACTGAGAGTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 442
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Db      1156 AATCTGAGAGAACTGAGAGGCTCAGGGTGTGATTAACATTTTAAAGTTAACGAGAAATC 1215
      1096 GACAACTTCTACCTCTAGAGGCTTTCACCTACCAAAATGTGGCTCTGGAGTGAAGTGC 1155
      1216 GATTAATTTTCTTCTGCTTATTTGGATATCAATACATCCGAGTCTAGCATAAAGAGAC 1275
Qy      1156 GCCCAGCTCTGCTCCGCTAGAGAGAGACGACCGCTTCATTGAGGCTGCAAGACACAG 1215
      1276 ACAGACCTCTCTGCGCCACATGGAATGAGCGTATCAATTTTAAACAAAGCGAAGAGAAC 1335
Qy      1216 GGCACCCACGCTGTGTCTCCACTGCAAGATGGGCGCTCAGCGGCTCAGCGGCCACAGTGTG 1275
      1336 CATTCGAATGCTGTGTGTGATTTGCAAAATGGGCGTGAAGTCTGAGCTCCACAGTCATA 1395
Qy      1276 GCTATGCAATGAGAGATTCGAGTGGCTCTGAAAAAGCATATATGTAAGACAG 1455
      1396 GCTATGCAATGAGAGATTCGAGTGGCTCTGAAAAAGCATATATGTAAGACAG 1455
Qy      1336 CTCGGCCCATGCGCCGCGCCCAACCTGTGCTTCTGCGCAAGTGCAGATCTACAGAGGC 1395
      1456 AAGCGAGCATACGCGCCCAACGCGGCTTTATGAGGCACTGTCTGAGTATGAAAGGC 1515
Qy      1396 ATCTGACGCGCCAGCGCCAGACCA 1421
      1516 ATCTTGATGCAAGCAACAGCGGCA 1541
Db

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RESULT 14
US-10-363-676-9
; Sequence 9, Application US/10363676
; Publication No. US20030170856A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN MAP KINASE PHOSPHATASE-LIKE ENZYME
; FILE REFERENCE: L10122 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/363,676
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/230,709
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patemcin version 3.1
; SEQ ID NO 9
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-363-676-9

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```

Query Match      18.0%; Score 356.4; DB 13; Length 494;
Best Local Similarity 98.4%; Pred. No. 2.7e-83;
Matches 360; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1159 CGCACTGAGAGAGAGAGAGAGCGCTTCATTGAGGCTGCAAGAGACAGAGGCAACCAAGTGC 1228
      1 CGCACTGAGAGAGAGAGAGAGCGCTTCATTGAGGCTGCAAGAGACAGAGGCAACCAAGTGC 60
Db
Qy      1229 TGGTCACTGCAAGATGAGGCGCTGACCGCTGACGCGCCACAGTGTGCTTATGCAATGA 1288
      61 TGGTCACTGCAAGATGAGGCGCTGACCGCTGACGCGCCACAGTGTGCTTATGCAATGA 120
Db
Qy      1289 AGCAATAGCAATGAGCGCTGAGAGAGGCGCTGCGCCAGAGTGTGCGGCCATCG 1348
      121 AGCAATAGCAATGAGCGCTGAGAGAGGCGCTGCGCCAGAGTGTGCGGCCATCG 180
Db
Qy      1349 CCGGCGCCCAACCTGCTTCTGCGCGCAGCTGCAAGATTCACAGGGCATCTCTGAGGCA 1408
      181 CCGGCGCCCAACCTGCTTCTGCGCGCAGCTGCAAGATTCACAGGGCATCTCTGAGGCA 240
Db
Qy      1409 GCGGCGCAAGCATCTCTGAGAGAGAAAGTGGTGGGCTCTCCCAAGAGAGACCCAG 1468
      241 GCGGCGCAAGCATCTCTGAGAGAGAAAGTGGTGGGCTCTCCCAAGAGAGACCCAG 300
Qy      1469 CCGCTGAAGTCTCTACCATCTCCACCTCTTCGCGCCAGAACCTGAGGGTGTGGGAGG 1528

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Db      301 CCGCTGAAGTCTTACACCATCTCCACCTCTCGCCAGAAACCTGAGGGTGTGGCGTGC 360
Qy      1529 AGAGG 1534
Db      361 GGGGGG 366

RESULT 15
US-09-775-925-1
; Sequence 1, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1949
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-775-925-1

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Query Match      17.2%; Score 340.4; DB 9; Length 1949;
Best Local Similarity 59.5%; Pred. No. 5.1e-79;
Matches 597; Conservative 0; Mismatches 401; Indels 6; Gaps 1;

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Qy      424 GATGAGACGCTCTCTCTGCGCGCTGAGTTTCTCTGACAGACAGCTCCCCAGCTGCACCTG 483
      32 GAGAGATATCTTCTGCTGGAGTGAATTTCCAGTAAAGAAATGAAGCTGCACCATTT 91
Db
Qy      484 GGCCTGCTTCTGCGCCCTCTGAGTGAACCCAGAGTACTTATGAGAGAGCGGGGCTTC 543
      92 GCGAGTGTCTTCCGACTGTGAGAGAGAGAGAAATCCACTTATGAGTGTGAGTTC 151
Db
Qy      544 AGCGTACGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603
      152 AGCGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 211
Db
Qy      604 GCGACATCCAGGATTTGACCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
      212 TCTGCGCTGAGGAGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
Db
Qy      664 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723
      272 GGGGGTGTAGCTCTCACTGAGGCTTCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
Db
Qy      724 TGGCTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
      332 TGGCTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
Db
Qy      784 C-----CTGCGCGGCTCTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
      392 CTATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
Db
Qy      838 TGAAGAGTGTGATGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897
      452 CGAAGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
Db
Qy      898 CTGAGAGTGGCGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
      512 TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
Db
Qy      958 CTGCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017
      572 CTACTTATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
Qy      1018 TCAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077

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Db      632 |TGTGATGGAATGCTCCAAATGTGAGAACTGCAGGGCTCAGGGTTGATTACATTTTA 691
Qy      1078 AACATGCCCCGGGAGATTGACAACTTCTACCTGAGCGCTTCACCTACCAACATGTGGC 1137
Db      692 AATGTTACGAGAAATCGATAATTTTCTCTGCTTAATTGCAATATCATATACATCCGA 751
Qy      1138 CTCTGGATGAGAGATTCGGCCCGAGTGTGCTGCGGCACTGGAAAGAGAGACGACCGCTCAT 1197
Db      752 GTCTACGATGAGAGACCAAGACCTCTCTGCGCCACGTGAAATGAAGCTATCATTTTATA 811
Qy      1138 GAGCTGCAAGAGCAAGGCAAGGCAAGGCTGCTGTCACTGCAAGATGGGCGTCAGCCGC 1257
Db      812 AACAAAGGGAAGAGAACCATTCGAAGTGGCTGTGCATGCAAAATGGCGGTGAGTCGC 871
Qy      1258 TCAGCGGCCACAGTGTGCTGCTATGCCATGAAGCAGTACGATGAGCCTGAGAGAGGCC 1317
Db      872 TGGGCTTCCACAGTCATAGCTATGCAATGAAGGAAATGGGCTGCTCTTGAAAAAGCA 931
Qy      1318 CTGGCGCAAGTGCAGGAGCTCCGGCCCATCGCCCGCCCAACCTGAGCTTCTTGCGCCAG 1377
Db      932 TATACTATGTAAAGCAGAGGCGACATCAAGCGCCCAAGCGGCTTTATGAGGCAG 991
Qy      1378 CTGCAGATCTACAGGCGCATCTCTGAGGCGCAGCCCGCAGAGCCA 1421
Db      992 CTGTCTGAGTATGAAGGCGCATCTTGATGCAAGCAAAACAGCGGCA 1035
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Job time : 671 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 15:07:05 ; Search time 143 Seconds

(without alignment)
611.459 Million cell updates/sec

Title: US-09-955-732-1

Perfect score: 1980
Sequence: 1 atgagccctgctacagctgag.....gagagagagagagagcctga 1980

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/ECTUS.COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1 | 101.8 | 5.1 | 531 | US-09-704-139-3 | Sequence 3, Appli |
| 2 | 101.8 | 5.1 | 1390 | US-09-704-139-1 | Sequence 1, Appli |
| 3 | 85.4 | 4.3 | 1238 | US-08-530-290-11 | Sequence 11, Appli |
| 4 | 85.4 | 4.3 | 1238 | US-09-702-705-803 | Sequence 803, App |
| 5 | 85.4 | 4.3 | 1238 | US-09-736-457-803 | Sequence 803, App |
| 6 | 85.4 | 4.3 | 2064 | US-09-702-705-825 | Sequence 825, App |
| 7 | 85.4 | 4.3 | 2064 | US-09-736-457-825 | Sequence 825, App |
| 8 | 85.4 | 4.3 | 2109 | US-09-702-705-826 | Sequence 826, App |
| 9 | 85.4 | 4.3 | 2109 | US-09-736-457-826 | Sequence 826, App |
| 10 | 85.4 | 4.3 | 2240 | US-09-016-434-1100 | Sequence 1100, App |
| 11 | 85.4 | 4.2 | 2303 | US-09-922-146-3 | Sequence 3, Appli |
| 12 | 83.8 | 4.2 | 1619 | US-09-702-705-801 | Sequence 801, App |
| 13 | 83.8 | 4.2 | 1619 | US-09-736-457-801 | Sequence 801, App |
| 14 | 83.8 | 4.2 | 4637 | US-09-702-705-804 | Sequence 804, App |
| 15 | 83.8 | 4.2 | 4637 | US-09-736-457-804 | Sequence 804, App |
| 16 | 83.8 | 4.2 | 2347 | US-09-016-434-864 | Sequence 864, App |
| 17 | 81.4 | 4.1 | 2377 | US-09-920-668-3 | Sequence 3, Appli |
| 18 | 77.4 | 3.9 | 1987 | US-08-990-379-1 | Sequence 1, Appli |
| 19 | 77.4 | 3.9 | 1993 | US-08-990-379-2 | Sequence 2, Appli |
| 20 | 73.6 | 3.7 | 1830 | US-09-557-921-1 | Sequence 1, Appli |
| 21 | 71.2 | 3.6 | 2109 | US-09-016-434-1135 | Sequence 1135, App |
| 22 | 70.6 | 3.5 | 2000 | US-09-016-434-1191 | Sequence 1191, App |
| 23 | 68.4 | 3.5 | 944 | US-09-371-671B-10 | Sequence 10, Appli |
| 24 | 65.6 | 3.3 | 539 | US-09-389-681-311 | Sequence 311, App |
| 25 | 65.6 | 3.3 | 539 | US-09-620-405B-311 | Sequence 311, App |
| 26 | 65.6 | 3.3 | 539 | US-09-339-338-311 | Sequence 311, App |
| 27 | 65.6 | 3.3 | 539 | US-09-433-826B-311 | Sequence 311, App |

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| C | 28 | 65.6 | 3.3 | 539 | 4 | US-09-604-287A-311 | Sequence 311, App |
| | 29 | 65 | 3.3 | 2450 | 4 | US-09-770-595A-21 | Sequence 21, Appli |
| | 30 | 61.6 | 3.1 | 1729 | 3 | US-09-045-973-6 | Sequence 6, Appli |
| | 31 | 56.2 | 2.8 | 594 | 3 | US-09-163-833-3 | Sequence 3, Appli |
| | 32 | 56.2 | 2.8 | 912 | 3 | US-09-163-833-1 | Sequence 1, Appli |
| | 33 | 55.8 | 2.8 | 1227 | 4 | US-09-620-312D-1027 | Sequence 1027, App |
| | 34 | 54.6 | 2.8 | 1380 | 4 | US-09-620-312D-1026 | Sequence 1026, App |
| | 35 | 53.2 | 2.7 | 1691 | 3 | US-09-013-881-12 | Sequence 12, Appli |
| | 36 | 53.2 | 2.7 | 1691 | 4 | US-09-612-473-12 | Sequence 12, Appli |
| | 37 | 53.2 | 2.7 | 1878 | 4 | US-09-620-312D-398 | Sequence 398, App |
| | 38 | 52.6 | 2.7 | 216 | 2 | US-08-530-290-9 | Sequence 9, Appli |
| | 39 | 51.6 | 2.6 | 1491 | 2 | US-09-544-716-1 | Sequence 1, Appli |
| | 40 | 50.2 | 2.5 | 861 | 1 | US-07-988-273-1 | Sequence 1, Appli |
| | 41 | 50.2 | 2.5 | 861 | 5 | PCT-US93-12019-1 | Sequence 1, Appli |
| | 42 | 48.6 | 2.5 | 477 | 3 | US-09-135-594-1 | Sequence 1, Appli |
| | 43 | 48.6 | 2.5 | 477 | 4 | US-09-684-843A-1 | Sequence 1, Appli |
| | 44 | 48.2 | 2.4 | 237 | 2 | US-08-530-290-8 | Sequence 8, Appli |
| | 45 | 48 | 2.4 | 3889 | 4 | US-09-484-970B-39 | Sequence 39, Appli |

ALIGNMENTS

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RESULT 1
US-09-704-139-3
Sequence 3, Application US/09704139
Patent No. 6420153
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosanna
TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
FILE REFERENCE: 10448-018001
CURRENT APPLICATION NUMBER: US/09/704,139
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/185,772
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapiens
US-09-704-139-3

Query Match 5.1%; Score 101.8; DB 4; Length 531;
Best Local Similarity 52.8%; Pred. No. 5.1e-14;
Matches 220; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

991 CGCATCTTCCCGCCACCTCTTACCTGCGCTCAGATGGAACGACCAACTGAGAGCTG 1050
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1111 GAGCGTTTCACTTACCAATGATGCGCTTGTGATGATGAGATGCGCCAGCTGCTCCG 1170
181 CCCGCGCTGCGAGAGCTGCGCGCTGCTTGTGACACCCCGGCTGAGACTGCTGCGCG 240
1171 CACTGGAAGAGAGCGACCGCTTATGTAGAGCTGCAAGACACAGGCGACCAACGCGCTG 1230
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1231 GTCCACTGCAAGATGGCGCTCAGCGCTGCAAGCGCCACAGTGTGCGCTTATGCAATGA 1290
301 GTTACTGCAAGAACGCGCGCGCTGCGCGCTGCGCGCTGCAAGCGCGCTGCTGCTGCGG 360
1291 CAGTACCAATGCAAGCTGAGAGAGCGCGCTGCGCGCTGAGAGAGCTGCGCGCTGCGG 1350
361 CACGCGCGCTGAGCGCTGCGGAGAGCGCTTCAATGATGATGAGAGCGCTGCGCGTGA 420
1351 CGCCCAACCTGAGCTTCTGCGCGCGCTGAGAGCTGCAATGATGAGAGCGCTGAGAGCG 1407
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Db 421 GAACCAACCCGGGCTTCTGCTCAGCTCCAGAAATATAGAGAGGCCCTCCAGGCC 477

RESULT 2

US-09-704-139-1

Sequence 1, Application US/09704139
 Patent No. 6420153
 GENERAL INFORMATION:
 APPLICANT: Kapeller, Rosanna
 TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
 FILE REFERENCE: 10448-018001
 CURRENT APPLICATION NUMBER: US/09/704,139
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: US 60/185,772
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 1
 LENGTH: 1390
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (329)..(859)
 NAME/KEY: misc.feature
 LOCATION: (1)..(1390)
 OTHER INFORMATION: n = a, t, g, or c
 US-09-704-139-1

Query Match 5.1%; Score 101.8; DB 4; Length 1390;
 Best Local Similarity 52.8%; Pred. No. 6.7e-14;
 Matches 220; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 991 CGCATCTTCCCGCCACTCTACCTGAGCTGAGTGAAGCAAGCAAACTTGAGAGAGCTG 1050
 DB 389 CGGCTGCGGCTTCACTCTTCTCGGAGCGCCGCGCGCGCGAGAGAGAGCTG 448
 QY 1051 CAGAGGAACAGGGTCAACCAATCTTGAACATGCGCGGAGATTGACACTTCTACCT 1110
 DB 449 GCGCGCGGGAGTCACTGCTGCTCAAGTCTCCGCGCAGAGCCGCGCGCGCG 508
 QY 1111 GAGCGCTTCACTTCAACCAATGCGGCTTGGAGTGAAGAGTCCGCGCGAGCTGCGG 1170
 DB 509 CCGCGGTGAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 568
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RESULT 3

US-08-530-290-11

Sequence 11, Application US/08530290
 Patent No. 5958721
 GENERAL INFORMATION:
 APPLICANT: Marshall, Christopher John
 APPLICANT: Ashworth, Alan
 APPLICANT: Hughes, David Anthony
 TITLE OF INVENTION: Methods for Screening of Substances for
 TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
 NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/530,290

FILING DATE: 14-DEC-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/GB94/00694

FILING DATE: 31-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9402573.1

FILING DATE: 10-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9307250.2

FILING DATE: 07-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 084611-000000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1238 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-530-290-11

Query Match 4.3%; Score 85.4; DB 2; Length 1238;
 Best Local Similarity 50.4%; Pred. No. 3.1e-10;
 Matches 209; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 994 ATCTTCCCGCCACTCTTCTGCGCTGAGTGAAGCAAGCAAACTTGAGAGAGCTGCGG 1053
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 QY 1054 AGAAGAGAGGAGCCAGCATCTTGAACATGAGCGCGGAGATTGACAACTTCTACCTGAG 1113
 DB 708 GCGCTGAGCATCAGGCTCTGTTGATGCTCTCTCGAGCTGCCCAAAACACTTTGAAGGA 767
 QY 1114 CGCTTCACTTACCAAAATGTCGCGCTTGGAGTGAAGAGTGGCCCAAGCTGCTGCGGAC 1173
 DB 768 CACTATAGATGAAGTGCATCCAGTGAAGATTAACCAAGAGCGCAGCATCAAGCTCTG 827
 QY 1174 TGAAGAGAGAGCAGCGCTTCACTTGAAGCTGCAAGAGCAGAGGCAAGGCGAGCTGCTG 1233
 DB 828 TTCTATGAAGCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 887
 QY 1234 CACTGAAGATGAGCGCTGAGCGCGCTGAGCGCGCAGAGTGTGCGCTATGCAATGAACAG 1293
 DB 888 CACTGCAAGGAGGAGCATCTGCGCGTGGCGCAGCATCTGCTGAGTGAATGATGAG 947
 QY 1294 TACAAATGAGCGCTGAGAGAGCGCTTGGCAGTGAAGAGTCCGCGCGCATGCGCGCG 1353
 DB 948 AAAGGGTGAAGGTGAGAGAGCGCTTGAAGTGTGTTAAGAGAGCGCGCAGACATCATTCG 1007
 QY 1354 CCGAACCCTGCTCTGCGCGCAGCTGAGATCTACAGGAGCATCTGAGCGGCA 1408
 DB 1008 CCGAATTCAGCTTCAAGGAGAGCTGCTGAGTGAAGTCCAGAGGTGCGCA 1062

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RESULT 4
US-09-702-705-803
; Sequence 803, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-803

Query Match      4.3%; Score 85.4; DB 4; Length 1238;
Best Local Similarity 50.4%; Pred. No. 3.1e-10;
Matches 209; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 994 ATCTTCCCCCACTCTTACCTGGGCTCAGAGTGAAGGACGCAAACTGGAGAGCTGCAG 1053
DB 648 ATCTTCCCCCTCTCTTACCTCGGAGTGCCTACATGCTCCCGAGAGACATGCTGCAGC 707
QY 1054 AGGAACAGGGGTCAACCCACATCTTGAACATGAGCCCGGAGATGACAACTTACCTGAG 1113
DB 708 GCCCTGGGATCAGCGCTCTGTGAATGTCTCTCTGGAGTCCCGCAACACCTTGAAGA 767
QY 1114 CGCTTACCTACCAATATGTGGCTCTGGATGAGAGTGGCCAGCTGTGCCGAC 1173
DB 768 CACTATCAGTACAGATGATCCAGGAGATTAACCAAGGCGAGCATGCTCTCG 827
QY 1174 TGAAGAGACGACCGCTTATTTAGGCTGCAAGAGCAGGAGACCCAGCTGTGTC 1233
DB 828 TTCAATGGAAGCATAGATGATCGATGCTGGAAGAGACTGCCGTGGGCGCTGTGTC 887
QY 1234 CACTGCAAGATGGGCTCAGCGCTCAGCGGCAAGTGTGGCTATGCCATGAAGCAG 1293
DB 888 CACTGCGAGGCGGATCTCGCGGTGGCCACCATCTGCTGCTATCTGATGAG 947
QY 1294 TACGAATGACGCTGAGAGAGGCGCTGCGGCCACGTCGAGAGACTCCGCCCATGCCCGC 1353
DB 948 AAACGGGTAGGCTGAGAGAGGCTTGCAGTTGTAAAGACAGCGCGCATCATCTCG 1007
QY 1354 CCCAACCTGAGCTTCTCTGCGCCAGCTGACAGATCTACAGGGGATCTTGACGCCCA 1408
DB 1008 CCCAATTGAGCTTCAATGGGCGAGCTGCTGCAAGTTCAGAGTGTGTCGCCA 1062

RESULT 5
US-09-736-457-803
; Sequence 803, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
```

```
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-803

Query Match      4.3%; Score 85.4; DB 4; Length 1238;
Best Local Similarity 50.4%; Pred. No. 3.1e-10;
Matches 209; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 994 ATCTTCCCCCACTCTTACCTGGGCTCAGAGTGAAGGACGCAAACTGGAGAGCTGCAG 1053
DB 648 ATCTTCCCCCTCTCTTACCTCGGAGTGCCTACATGCTCCCGAGAGACATGCTGCAGC 707
QY 1054 AGGAACAGGGGTCAACCCACATCTTGAACATGAGCCCGGAGATGACAACTTACCTGAG 1113
DB 708 GCCCTGGGATCAGCGCTCTGTGAATGTCTCTCTGGAGTCCCGCAACACCTTGAAGA 767
QY 1114 CGCTTACCTACCAATATGTGGCTCTGGATGAGAGTGGCCAGCTGTGCCGAC 1173
DB 768 CACTATCAGTACAGATGATCCAGGAGATTAACCAAGGCGGAGCATGCTCTCG 827
QY 1174 TGAAGAGACGACCGCTTATTTAGGCTGCAAGAGCAGGAGACCCAGCTGTGTC 1233
DB 828 TTCAATGGAAGCATAGATGATCGATGCTGGAAGAGACTGCCGTGGGCGCTGTGTC 887
QY 1234 CACTGCAAGATGGGCTCAGCGCTCAGCGGCAAGTGTGGCTATGCCATGAAGCAG 1293
DB 888 CACTGCGAGGCGGATCTCGCGGTGGCCACCATCTGCTGCTATCTGATGAG 947
QY 1294 TACGAATGACGCTGAGAGAGGCGCTGCGGCCACGTCGAGAGACTCCGCCCATGCCCGC 1353
DB 948 AAACGGGTAGGCTGAGAGAGGCTTGCAGTTGTAAAGACAGCGCGCATCATCTCG 1007
QY 1354 CCCAACCTGAGCTTCTCTGCGCCAGCTGACAGATCTACAGGGGATCTTGACGCCCA 1408
DB 1008 CCCAATTGAGCTTCAATGGGCGAGCTGCTGCAAGTTCAGAGTGTGTCGCCA 1062

RESULT 6
US-09-702-705-825
; Sequence 825, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 825
; LENGTH: 2064
; TYPE: DNA
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 QY 1294 TAGAATGACAGCTTGAGAGAGGCGCTTGGCCAGATGACAGACTTGGGCGCCATGGCCGC 1353
 Db 1251 AAACGGGTGAGGTGAGAGAGGCGCTTGGAGTTGTTAAGCAGAGCGCCAGCATCTGCG 1310
 QY 1354 CCCAACCTTGCTTCTGCGCCAGCTGACAGATCTACAGAGGCAATCTGACGCGCA 1408
 Db 1311 CCCAATTGAGCTTCAATGGGCGAGCTGCTGCACTTGAATCCAGAGTGTGTGCGCA 1365

RESULT 9

US-09-736-457-826
 ; Sequence 826, Application US/09736457
 ; Patent No. 6509448
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Wang, Aljun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/736,457
 ; CURRENT FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 1864
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 826
 ; LENGTH: 2109
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-736-457-826

Query Match 4.3%; Score 85.4; DB 4; Length 2109;
 Best Local Similarity 50.4%; Pred. No. 3.6e-10;
 Matches 209; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 994 ATCTTCCCCCACTCTTACCTGGGCTCAGAGTGAAGCGCAACCTGAGAGAGCTGCG 1053
 Db 951 ATCTTCCCCCTTCTCTTACCTGGGAGTGTCTACCATGCTGCCGAGAGACATGCTGAC 1010
 QY 1054 AGAAGAGGGTCAACCCACATCTTGAACATGCGCCGGAGATTGACAATTCTTACCTGTAG 1113
 Db 1011 GCCCTGGGATCACGGGCTGTGTAATGCTCTCGGACTGCCCAACCATTTGAAGA 1070
 QY 1114 CGCTTCACTTACCAATGTGCGCTCTGGAGTGAAGTGGCCCACTGCTGCCGAC 1173
 Db 1071 CACTATCAGTACAAGTGCATCCAGTGAAGATMACACAAGGCCCACTACAGCTCTGG 1130
 QY 1174 TGAAGAGAGCGACCGCTTATTGAGGCTGCAAGAGCAAGAGGCAACCCAGCTGCTGTC 1233
 Db 1131 TTATGAGAGCCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1190
 QY 1234 CACTGCAAGTGGGCTCAGCGGCTGAGCGGCCACAGTGTGCTATGCCATGAAGAG 1293
 Db 1191 CACTGCAAGGCGGATCTGCGGCTGAGCCACCATCTGCTGCTATGATGAAG 1250
 QY 1294 TAGAATGACAGCTTGAGAGAGGCGCTGCGCAGTGCAGAGAGTGGCGCCATGCGCCGC 1353
 Db 1251 AAACGGGTGAGGTGAGAGAGGCGCTTGGAGTTGTTAAGCAGAGCGCCAGCATCTGCG 1310
 QY 1354 CCCAACCTTGCTTCTGCGCCAGCTGACAGATCTACAGAGGCAATCTGACGCGCA 1408
 Db 1311 CCCAATTGAGCTTCAATGGGCGAGCTGCTGCACTTGAATCCAGAGTGTGTGCGCA 1365

RESULT 10

US-09-016-434-1100
 ; Sequence 1100, Application US/09016434
 ; Patent No. 6509318
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HERewith

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1100:
 SEQUENCE CHARACTERISTICS:

LENGTH: 2240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 91255784

US-09-016-434-1100

Query Match 4.3%; Score 85.4; DB 4; Length 2240;
 Best Local Similarity 50.4%; Pred. No. 3.7e-10;
 Matches 209; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 994 ATCTTCCCCCACTCTTACCTGGGCTCAGAGTGAAGCGCAACCTGAGAGAGCTGCG 1053
 Db 714 ATCTTCCCCCTTCTCTTACCTGGGAGTGTCTACCATGCTGCCGAGAGACATGCTGAC 773
 QY 1054 AGAAGAGGGTCAACCCACATCTTGAACATGCGCCGGAGATTGACAATTCTTACCTGTAG 1113
 Db 774 GCCCTGGGATCACGGGCTGTGTAATGCTCTCGGACTGCCCAACCATTTGAAGA 833
 QY 1114 CGCTTCACTTACCAATGTGCGCTCTGGAGTGAAGTGGCCCACTGCTGCCGAC 1173
 Db 834 CACTATCAGTACAAGTGCATCCAGTGAAGATMACACAAGGCCCACTACAGCTCTGG 893
 QY 1174 TGAAGAGAGCGACCGCTTATTGAGGCTGCAAGAGCAAGGSCACCCAGCTGCTGTC 1233
 Db 894 TTATGAGAGCCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 953
 QY 1234 CACTGCAAGTGGGCTCAGCGGCTGAGCGGCCACAGTGTGCTATGCCATGAAGAG 1293
 Db 954 CACTGCAAGGCGGATCTGCGGCTGAGCCACCATCTGCTGCTATGATGATGAAG 1013
 QY 1294 TAGAATGACAGCTTGAGAGAGGCGCTTGGAGTTGTTAAGCAGAGCGCCAGCATCTGCG 1365

ORGANISM: Homo sapien
US-09-736-457-801

Query Match 4.2% Score 83.8; DB 4; Length 1619;
Best Local Similarity 50.1%; Pred. No. 7.7e-10;
Matches 208; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 994 ATCTTCCCTCCACTTACCTGAGTGAAGAGCAAGCAAACTGAGAGAGTGCAG 1053
DB 320 ATCTTCCCTTCTCTACTGCGAGTGTCTACCAATGCTGCCGAGAGACATGCTGAC 379
QY 1054 AGAAGAGAGTCAACCAATCTTGAACATGCGCGGAGATTGAACACTTCTACCTTAG 1113
DB 380 GCCCTGGGATACAGGCTCTGTGAATGCTCTCGAGTGCCTCAACCACTTTGMAAGA 439
QY 1114 CGCTTCACTTACCAATATGCGCTCTGGAGTGAAGAGTGGCGCCAGTGTGCGGAC 1173
DB 440 CACTATCAATACATAGTCACTCCAGTGAAGATTAACCAAGCCGACATCACTCTCG 499
QY 1174 TGAAGAGAGAGCCAGCTTCAATGAAGCTGCAAGAGCAAGGCAACCTGCTGTC 1233
DB 500 TTCAATGAGAGCCATAGATCAATGCTGGAAGAGTGCCTGCGGCGCTGCTGCTG 559
QY 1234 CACTGAGAGATGGGGGTGAGCGCTGAGGGGCAAGTGTGGCTATGCCATGAGAG 1293
DB 560 CACTGCGAGCGGGGATCTCGGCTGCGGCACTCTGCTGCTGCTGCTGCTGCTGCTG 619
QY 1294 TAGGAATGAGAGCTTGAAGAGAGAGCTGCGGCACTGAGAGAGTCTGCGCCAG 1353
DB 620 AAACGGGTAGGCTGAGAGAGGCTTCAAGTTCGTTAAGAGCGCGGAGATTAATCTG 679
QY 1354 CCCAACCTGCTTCTGCGGCACTGAGATCTACCGGAGATCTTGAAGAGCA 1408
DB 680 CCCAATTGAGCTTATGAGGAGCTGTGAGATTCGAGTCCAGTCTGCGCA 734

RESULT 14

US-09-702-705-804
Sequence 804, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriek
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702.705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 804
LENGTH: 4637
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-804

Query Match 4.2% Score 83.8; DB 4; Length 4637;
Best Local Similarity 50.1%; Pred. No. 1e-09;
Matches 208; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 994 ATCTTCCCTCCACTTACCTGAGTGAAGAGCAAGCAAACTGAGAGAGTGCAG 1053
DB 320 ATCTTCCCTTCTCTACTGCGAGTGTCTACCAATGCTGCCGAGAGACATGCTGAC 379
QY 1054 AGAAGAGAGTCAACCAATCTTGAACATGCGCGGAGATTGAACACTTCTACCTTAG 1113

DB 380 GCCCTGGGATACAGGCTCTGTGAATGCTCTCGGAGTGCCTCAACCACTTTGAAGA 439
QY 1114 CGCTTCACTTACCAATATGCGCTCTGGAGTGAAGAGTGGCGCCAGTGTGCGGAC 1173
DB 440 CACTATCAATACATAGTCACTCCAGTGAAGATTAACCAAGCCGACATCACTCTCG 499
QY 1174 TGAAGAGAGAGCCAGCTTCAATGAAGCTGCAAGAGCAAGGCAACCACTGCTGTC 1233
DB 500 TTCAATGAGAGCCATAGATCAATGCTGGAAGAGTCCGCTGAGAGACTGCGGCGCTGCTG 559
QY 1234 CACTGAGAGTGGGCTGAGCGCTGAGCGGCAAGTGTGCTGCTTATGCCATGAAGAG 1293
DB 560 CACTGCGAGCGGGGATCTCGGCTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 619
QY 1294 TAGGAATGAGAGCTTGAAGAGAGAGCTGCGGCACTGAGAGAGTCCGCGCCATGCGCGC 1353
DB 620 AAACGGGTAGGCTGAGAGAGGCTTCAAGTTCGTTAAGAGCGCGGAGATTAATCTG 679
QY 1354 CCCAACCTGCTTCTGCGGCACTGAGATCTACCGGAGATCTTGAAGAGCA 1408
DB 680 CCCAATTGAGCTTATGAGGAGCTGTGAGATTCGAGTCCAGTCTGCGCA 734

RESULT 15

US-09-736-457-804
Sequence 804, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriek
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736.457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 804
LENGTH: 4637
TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-804

Query Match 4.2% Score 83.8; DB 4; Length 4637;
Best Local Similarity 50.1%; Pred. No. 1e-09;
Matches 208; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 994 ATCTTCCCTCCACTTACCTGAGTGAAGAGCAAGCAAACTGAGAGAGTGCAG 1053
DB 320 ATCTTCCCTTCTCTACTGCGAGTGTCTACCAATGCTGCCGAGAGACATGCTGAC 379
QY 1054 AGAAGAGAGTCAACCAATCTTGAACATGCGCGGAGATTGAACACTTCTACCTTAG 1113
DB 380 GCCCTGGGATACAGGCTCTGTGAATGCTCTGGAATGCTGCGCAAACTTTGAAGA 439
QY 1114 CGCTTCACTTACCAATATGCGCTCTGGAGTGAAGAGTGGCGCCAGTGTGCGGAC 1173
DB 440 CACTATCAATACATAGTCACTCCAGTGAAGATTAACCAAGCCGACATCACTCTCG 499
QY 1174 TGAAGAGAGAGCCAGCTTCAATGAAGCTGCAAGAGCAAGGCAACCACTGCTGTC 1233
DB 500 TTCAATGAGAGCCATAGATCAATGCTGGAAGAGTCCGCTGAGAGACTGCGGCGCTGCTG 559
QY 1234 CACTGAGAGTGGGCTGAGCGCTGAGCGGCAAGTGTGCTGCTTATGCCATGAAGAG 1293

Db 560 CACTCCAGCGGGGATCTCGGGTCGGCCACCACTGCTGGCCTAAGTATGATGAAG 619
 QY 1294 TACGATGCAAGCTTGAGAGAGGCGCTGCGCCACAGTGCAGAGCTCCGGCCATCGCCCGC 1353
 Db 620 AAACGGGTGAGGCTGAGAGAGGCTTCGAGTTCTTTAGAGAGCGCCGAGCATTTATCTCG 679
 QY 1354 CCCAACCTGCTTCTCGGCGAGCTGAGATCTACAGGGCATCTGACGGCCA 1408
 Db 680 CCCAATTGAGTTTCATGAGGCGAGCTGCGAGTTGAGTCCAGAGTGTGCGCA 734

Search completed: January 15, 2004, 18:31:49
 Job time : 146 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 15, 2004, 06:48:01 ; Search time 21 Seconds

(without alignments)
3017.865 Million cell updates/sec

Title: US-09-955-732-2

Perfect score: 3412

Sequence: 1 MALTVSRSPFGSGASTPVG.....RRKRVQASVHDSGESEA 659

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 269.5 | 7.9 | 220 | 2 JCT885 | low-molecular-mass |
| 2 | 224 | 6.6 | 384 | 1 I38890 | dual specificity p |
| 3 | 214 | 6.3 | 226 | 2 T21380 | hypothetical prote |
| 4 | 210.5 | 6.2 | 272 | 2 T18915 | hypothetical prote |
| 5 | 210.5 | 6.2 | 319 | 2 T15969 | hypothetical prote |
| 6 | 209.5 | 6.1 | 393 | 2 A56947 | dual specificity p |
| 7 | 209 | 6.1 | 394 | 2 B57126 | dual specificity p |
| 8 | 206.5 | 6.1 | 394 | 2 A56115 | dual specificity p |
| 9 | 204.5 | 6.0 | 303 | 2 A56405 | hypothetical prote |
| 10 | 202 | 5.9 | 314 | 2 A57126 | dual specificity p |
| 11 | 202 | 5.9 | 367 | 1 S29090 | dual specificity p |
| 12 | 196.5 | 5.8 | 223 | 2 I49365 | protein tyrosine p |
| 13 | 194.5 | 5.7 | 365 | 2 T32494 | hypothetical prote |
| 14 | 194 | 5.7 | 367 | 1 S24411 | dual specificity p |
| 15 | 194 | 5.7 | 367 | 1 S22265 | dual specificity p |
| 16 | 193 | 5.7 | 489 | 1 S58725 | dual specificity p |
| 17 | 188.5 | 5.5 | 205 | 2 I48314 | protein-tyrosine-p |
| 18 | 187 | 5.5 | 330 | 2 T39698 | protein tyrosine p |
| 19 | 186.5 | 5.5 | 185 | 1 A47191 | dual specificity p |
| 20 | 186.5 | 5.5 | 866 | 1 F88481 | protein C16A3.1 (1 |
| 21 | 185 | 5.4 | 283 | 2 G84458 | probable protein p |
| 22 | 179 | 5.2 | 142 | 2 T03074 | dual specificity p |
| 23 | 177.5 | 5.2 | 276 | 2 T48906 | protein-tyrosine-p |
| 24 | 176 | 5.1 | 2472 | 1 E83594 | still frameshift p |
| 25 | 173.5 | 5.1 | 364 | 1 S31304 | protein-tyrosine p |
| 26 | 169 | 5.0 | 186 | 2 T16056 | hypothetical prote |
| 27 | 155.5 | 4.6 | 4957 | 2 T03455 | ALR protein - huma |
| 28 | 155.5 | 4.6 | 5262 | 2 T03454 | ALR protein - huma |
| 29 | 154 | 4.5 | 292 | 2 S41012 | hypothetical prote |

| | | | | | |
|----|-------|-----|------|----------|--------------------|
| 30 | 153 | 4.5 | 580 | 2 T18439 | hypothetical prote |
| 31 | 153 | 4.5 | 600 | 2 T18446 | hypothetical prote |
| 32 | 143 | 4.2 | 771 | 2 T47666 | phosphatase-like p |
| 33 | 141 | 4.1 | 3938 | 2 T42761 | Bassoon protein - |
| 34 | 140.5 | 4.1 | 1805 | 2 A34736 | nestin - rat |
| 35 | 135.5 | 4.0 | 1571 | 2 T00062 | hypothetical prote |
| 36 | 135.5 | 4.0 | 1606 | 2 T34073 | paramerin - chicke |
| 37 | 133 | 3.9 | 1346 | 2 A57376 | probable regulator |
| 38 | 132.5 | 3.9 | 837 | 2 T02761 | outer arm dynein 1 |
| 39 | 131.5 | 3.9 | 807 | 1 S44538 | probable protein-t |
| 40 | 131.5 | 3.9 | 2175 | 1 S03170 | homeotic protein c |
| 41 | 130 | 3.8 | 990 | 2 T14756 | hypothetical prote |
| 42 | 130 | 3.8 | 1426 | 2 T00337 | hypothetical prote |
| 43 | 128.5 | 3.8 | 1186 | 2 G69708 | chromosome segrega |
| 44 | 128 | 3.8 | 209 | 1 S48459 | probable dual spec |
| 45 | 128 | 3.8 | 1366 | 2 B86292 | F7H2.12 protein - |

ALIGNMENTS

RESULT 1

UC7885 low-molecular-mass dual-specificity phosphatase-2 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003

C:Accession: UC7885

R:Nakamura, K.; Tanoue, K.; Sato, T.; Takekawa, M.; Watanabe, M.; Shima, H.; Kikuchi, K

J. Biochem. 132, 463-470, 2002

A:Title: A novel low-molecular-mass dual-specificity phosphatase, LDP-2, with a natural

A:Reference number: UC7885; MUID:22194259; PMID:12204117

A:Accession: UC7885

A:Molecule type: mRNA

A:Residues: 1-220 <NAK>

A:Cross-references: DDBJ:AB038769; DDBJ:AB038770

A:Comment: This enzyme, a novel member of the low-molecular-mass dual-specificity phosph

ein kinase signaling.

C:Genetics:

A:Gene: ldp-2

Query Match

Best Local Similarity

Matches 62; Conservative 30; Mismatches 58; Indels 13; Gaps 2;

7.9%; Score 269.5; DB 2; Length 220;

332 IFPHLYGSEWNAANLELORNRVTHLNNAREIDNFPERTYHNVRLMDESAQLPH 391

DB 68 IKPVLILGSDPAHDELKHKVTHLNVAYGVENAFLEFTYKITSIDVPERNTLSY 127

OY 392 WKETHRTLEAPACGTHLVHCKMGVRSAAVLAVMKQYEGSLDQLRHVOELRIAR 451

DB 128 FPECFEFIEQAKLDGVVLVHCNAGVRAAIVYGFMSSEETFTALSLVKEAPPSIC 187

OY 452 FNPGLRLOLYOGITLNASRQSHWEQKGVGVSEEPPEVDS 494

DB 188 FNPGLRLOLYOGITLNASRQSHWEQKGVGVSEEPPEVDS 494

188 FNPGLRLOLYOGITLNASRQSHWEQKGVGVSEEPPEVDS 494

188 FNPGLRLOLYOGITLNASRQSHWEQKGVGVSEEPPEVDS 494

188 FNPGLRLOLYOGITLNASRQSHWEQKGVGVSEEPPEVDS 494

Rishibashi, T.; Bottaro, D.P.; Micheli, P.; Kelley, C.A.; Aaronson, S.A.
 J. Biol. Chem. 269, 29897-29902, 1994
 A:Title: A novel dual specificity phosphatase induced by serum stimulation and heat shock
 A:Reference number: A55313; M0ID:95050849; PMID:7961985
 A:Accession: A55313
 A:Molecule type: mRNA
 A:Residues: 1-8, 'GHV', 12-70, 'R', 72-104, 'F', 107-362, 'RCLPQSGSAAELMORPANKTGMESNOPEQL
 A:Cross-references: GB:U15932; NID:9606971; PIDN:AAA64693.1; PID:9606972
 A:Experimental source: mammary epithelial cells
 C:Genetics:
 A:Gene: GDB:DUSP5
 A:Cross-references: GDB:385447
 A:Map position: 10q25-10q25
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
 C:Keywords: phosphoprotein; phosphoprotein phosphatase homology <VHL>
 F:186-317/Domain VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:263/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:269/Binding site: substrate phosphate (Arg) #status predicted

Query Match 6.6%; Score 224; DB 1; Length 384;
 Best Local Similarity 27.7%; Pred. No. 5.3e-07;
 Matches 62; Conservative 40; Mismatches 84; Indels 38; Gaps 5;

QY 287 DLESVTSKET--RQALELRLGIPL--QQYRDFIDQMLLVACRBRARIPPHLYLGEW 342
 DB 142 DYKPISEQEIESERALISQCGKRVNVSYRPAVD-----QGGVPEILPEFLYSAY 192
 QY 343 NNALELQNRNTHILNAREIDNPERFTYHNRLWDESAQLDPHMKETHRFIEAA 402
 DB 193 HASKCFPLNHLTALLNRSRTSECMTHLHKMIPVDSHTADISSHFOALIDFIDCV 252
 QY 403 RAGTHVLVCKMGVSRSAATVLAAMKQYECGLEALRHVOELPIARPNGFRLQCI 462
 DB 253 REKGKVLVHCEAGISRSPTICMAVLMKQFRLKEAFDIYIKRSMVSPNGGQLIQ 312
 QY 463 YGQILASRQSHWEKVGVSPEEHAPREVSPPEPLPPEPEG 506
 DB 313 YESEILP-----STP-NPQPPSCQG 331

RESULT 3
 T21380
 hypothetical protein F26A3.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21380
 R:McMurray, A.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19415
 A:Accession: T21380
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-226 <WIL>
 A:Cross-references: EMBL:Z78419; PIDN:CAB01700.1; GSPDB:GN00019; CESP:F26A3.4
 A:Experimental source: clone F26A3
 C:Genetics:
 A:Gene: CESP:F26A3.4
 A:Map position: 1
 A:Insertions: 117/2; 150/3; 186/3

Query Match 6.3%; Score 214; DB 2; Length 226;
 Best Local Similarity 29.7%; Pred. No. 1.1e-06;
 Matches 69; Conservative 40; Mismatches 87; Indels 36; Gaps 10;

QY 330 SRFFPHLYGSEWNAANLELQNRNTHILNAREIDNPERFTYHNRLWDESAQ-- 387
 DB 15 SEIVPGILFICGV-SALSKDEMKRKHKTTHINATTEVPN-RSLGDIQRTKMLLEDTPQTY 72
 QY 388 LPHMKETHRFIEAARQGTHTLVHCKMGVSRSAATVLAAMKQYEC-SLEQALRHVOEL 446
 DB 73 IYVHLDSQDQIALADSGKVLVHCVAGVSRASGICLAFLLK-YRCRNLREAYVLMKSK 131
 QY 447 RPIARPNGFRLQCIYQGITLASRQSHWEKVGVS-----SPEE-HPAEVSSTPPE 498

DB 132 RSNVRPRLGFWROLIAYEONV-----KENAGVRLVRDEAOEQLPDPVYLNIAIP 182
 QY 499 PLPEPPEGGGEKVEKVMESQAAPKEPGRPRINLRGVRSISLPEL 550
 DB 183 ARPASPE-----QENMTPDE---PRENRNGFSKRPRVLEPVMEM 221

RESULT 4
 T18915
 hypothetical protein C04F12.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18915
 R:Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19044
 A:Accession: T18915
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-272 <WIL>
 A:Cross-references: EMBL:Z81461; PIDN:CAB03837.1; GSPDB:GN00019; CESP:C04F12.8
 A:Experimental source: clone C04F12
 C:Genetics:
 A:Gene: CESP:C04F12.8
 A:Map position: 1
 A:Insertions: 53/1; 84/3; 204/2

Query Match 6.2%; Score 210.5; DB 2; Length 272;
 Best Local Similarity 24.3%; Pred. No. 2.4e-06;
 Matches 75; Conservative 38; Mismatches 129; Indels 67; Gaps 6;

QY 330 SRFFPHLYGSEWNAANLELQNRNTHILNAREIDNPERFTYHNRLWDESAQL 389
 DB 12 SEINDHLYL-SGAGVLKPDIKQKINMVAATTEBPSTYMQVDVTKRIEHPARLN 70
 QY 390 PHMKETHRFIEAARQGTHTLVHCKMGVSRSAATVLAAMKQYECGLEALRHVOELPI 449
 DB 71 EHPDVADKIRNKRKRGKTLVHCVAGVSRASALVMIVLVKHEMTLRQYVHYKARPI 130
 QY 450 ARPNGFRLQCIYQGITLASRQSHWEKVGVSPEEHAPREVSTPPE 488
 DB 131 IRPNVGFWMQVDYEKLR-----GTASVVMQTPPCDMPIPVVADIRRMQ 178
 QY 499 -----PLPEPPEGGGEKVEKVMESQAAPKEPGRPRINLRGVRSISLPEL 550
 DB 179 INREISHSLPSAOSASKQRA-----SASTYRPSVS 212
 QY 551 ESTSETSDMEPEVPSHSHSEEPLOPPQIARTKGGQVDRGQPLKRSQSVYTLQGS 610
 DB 213 ASSIATSLRPRAVSPS-----LPASIALTTSYSLF--SPAPTRKPRQSLFSMYS 263
 QY 611 VVAARTQAF 619
 DB 264 PRHNFSAF 272

RESULT 5
 T15969
 hypothetical protein F08B1.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15969
 R:Chisoe, S.
 submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of C. elegans cosmid F08B1.
 A:Reference number: Z18439
 A:Accession: T15969
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-619 <CHI>
 A:Cross-references: EMBL:U23178; NID:9726421; PID:9726422; PIDN:AAC46719.1; CESP:F08B1.1
 A:Experimental source: strain Bristol N2

C:Genetics:
A:Gene: CESP.F08B1.1
A:introns: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match
Best Local Similarity 20.9%; Pred. No. 7.6e-06; Length 619;

Matches 113; Conservative 66; Mismatches 198; Indels 163; Gaps 18;

QY 268 QGEMQCAIRAEIMKVLID---VSDLESTSKRIQALRLT-----GLPL----- 308
D 40 RELEEDTKFRSVMVLEEQDPVSSLPFPKKFKGLKLTLLTSSPTNSSSPSSPTNG 99
QY 309 -----QGYRDFID-----NOMLLVAGDRASRIFPHHYGSENNANLEEL 350
D 100 GKKQFPQYQPOLCESEBGMTRLPQISLPCLSQPTGDTTLTPINITYGSDISLDETWL 159
QY 351 QNRVTHILNMA-----REIDNFPERTYHNVRLMDESAQLPHMKETRFTEA 401
D 160 DALDLSVINLMTCKSKVCIEDKNFM-----RIPNDGYQELSLPYFMAYEPLEK 212
QY 402 ARAQGTIVLVCKMGVSRSAATVLAAMKQYECGLEQALRHVQELRPILRPFGRLQIQ 461
D 213 CRAGKCKDHIHCLAGISRPTLAISYIKRYMKGSDDAYRYKERRPSISPFTNMGQIL 272
QY 462 IYQGITL-----TASR-----QSHVWEQV-----QGVAPREHPA-- 490
D 273 EYENVLIKQHVLDYNQASPRHMDYGGSDLCPEKVPKASASNCVFRGTHDESSPSP 332
QY 491 -----PEVST-----PPP-----LPPPE 503
D 333 SVSEGSNASEPPTSSSASSTASAPSPMPTSEGTSSGTIVNNGKMTMDLGLBHR 392
QY 504 PEGGGEKXVGMEEQ-AAPKE-----PGR-----PRINLRGM 538
D 393 PAFGLPGRITGVNMLPSPSTELSRISNGPEALAPSTPIINPCNSITILVASS 452
QY 539 RSISLLEPSELLESTSETSDMEV-FSSHESHEEPL--QPPPOLANTKGGQCYDRPQ 594
D 453 REVILLTLPRASSSSSTSESPSPSSSESSSSSIVVENFPFASTEVPASSSISIPS 512
QY 595 PALKRSQSVVTLQGSVAVNRTQAFQEQGQGGGECISTGTRFRKVVQASVHDSG 654
D 513 ---GSGSTPASASSASRCRMKGFYKYSKXAPASTSTPASSTGTSRAAPBCLRSSG 569

RESULT 6

A:Accession: A56947
A:Title: dual specificity phosphatase (EC 3.1.3.-) HVH2 - rat

N:Alternate names: mitogen-activated protein kinase phosphatase 2
C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-1999
C:Accession: A56947

R:Mitra-Press, A.; Rim, C.S.; Yao, H.; Roberson, M.S.; Stock, P.J.S.
J:Biol. Chem. 270 14587-14596, 1995

A:Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression, an
A:Reference number: A56947; MUID:95301550; PMID:7782322

A:Accession: A56947
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-393 <MIS>

C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C:Keywords: phosphoprotein; phosphoric monoester hydrolase

F:202-333/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F:279/Active site: Cys (phosphocysteine intermediate) #status predicted

F:285/Binding site: substrate phosphate (Arg) #status predicted

Query Match
Best Local Similarity 6.1%; Score 209.5; DB 2; Length 393;

Matches 54; Conservative 27; Mismatches 70; Indels 19; Gaps 2;

QY 332 IFPHLYLGSENNANLEELQNRVTHILNMAEIDNFPERTYHNVRLMDESAQLDLP 391
D 198 IIPFLYLGSAVHAARDMDALGITALNVSSDCNHFEGHYQKICPVEDHKKADISSW 257

QY 392 WKETHRIEAPAAQGTIVLVCKMGVSRSAATVLAAMKQYECGLEQALRHVQELRPIL 451
D 258 FMEALIXIDAVKDCRGVILVHCQAGISRATICLAYLMMKKRVRLAEAFVKGRSITIS 317
QY 452 PNPGLQ-LQIYQGITLTAQRSHWQKQGVSPPEHPAPVSTPPPL 500
D 318 PNFSEMGQLQFESQVLTS-----CAEAASPSGCL 349

RESULT 7

A:Accession: B57126
A:Title: dual specificity phosphatase (EC 3.1.3.-) 2 - mouse

N:Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1
C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1998
C:Accession: B57126

R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Kruttsch, H.; Siebenlist, U.; Kell
Science 259 1763-1766, 1993

A:Title: PAC-1, a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7651221

A:Accession: B57126
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-314 <ROH>

C:Cross-references: GB:L11310
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity

C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase
C:Keywords: dual specificity phosphoprotein phosphatase homology <VH1>

F:180-311/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F:257/Active site: Cys (phosphocysteine intermediate) #status predicted

F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match
Best Local Similarity 6.1%; Score 209; DB 2; Length 314;

Matches 43; Conservative 33; Mismatches 53; Indels 0; Gaps 0;

QY 332 IFPHLYLGSENNANLEELQNRVTHILNMAEIDNFPERTYHNVRLMDESAQLDLP 391
D 176 IIPFLYLGSCNHSDDLQGLACGTALNVNVSACPNFEBLFHKSIPVDNQMVELISAW 235
QY 392 WKETHRIEAPAAQGTIVLVCKMGVSRSAATVLAAMKQYECGLEQALRHVQELRPIL 451
D 236 FOEASIPIDSKVSGRWVHCQAGISRATICLAYLQSHRVRLAEAPFVXORGVIS 295
QY 452 PNPGLROL 460
D 296 PNFSEMGQL 304

RESULT 8

A:Accession: A56115
A:Title: dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 4 - human

N:Alternate names: dual specificity phosphatase HVH2
C:Species: Homo sapiens (man)

C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 24-Apr-1998
C:Accession: A56115

R:Guan, K.L.; Butch, E.
J:Biol. Chem. 270 7197-7203, 1995

A:Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, which
A:Reference number: A56115; MUID:95221370; PMID:7555768

A:Accession: A56115
A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-394 <GUA>

A:Cross-references: GB:U21108
C:Genetics:

A:Gene: GDB:DUSP4; HVH2: MKP-2
A:Cross-references: GDB:433893

A:Map position: Bp21-8p11.2
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity

C:Keywords: phosphoprotein; phosphoric monoester hydrolase
F:203-334/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>

F:280/Active site: Cys (phosphocysteine intermediate) #status predicted

F:286/Binding site: substrate phosphate (Arg) #status predicted

Query Match 6.1%; Score 206.5; DB 2; Length 394;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches 82; Conservative 46; Mismatches 124; Indels 101; Gaps 7;

222 GGSALTWASHYERINSESCINENTAMADLESPPAPSPG----- 264
25 GGAGGTGSHGTLGLPSGKCL-----LIDCPFLAHSGVILGSVNRCNTVRR 76
QY 265 -----SSSEQ-----DQEQAIRAEIMKVLDSVDSLETSKEIRQALERLGLPQYDF 314
DB 77 AKGSVLEQIILPAEEVRARLRSGLYSAVIYDERSPPAESLIRE--DSTVLVQVALERN 134
QY 315 ID-NQMLLVQDRAS----- 330
DB 135 AERTDCLIKGGERSSSEYPPFCSTKALAAIPPPVPSPATPEPDLICSSCGTPIHDG 194
QY 331 ---RIFPHLYLGSEWNAANLELORNRVTHILNMAREIDNFPYPERFYHNVRLWDESAQ 387
DB 195 GPVEILPFLYLGSAVYAAARMDLALGITALLNVSDCPNHPGHYQKCIPEVDHNRAD 254
QY 388 LDPHMKETRRFTEAARQGTIVLVHCKMGVSRSATVLAAMKQYECSEQLRHVOELR 447
DB 255 ISSWFEEALEYIDAVDCRGVLVHCOAGISRSATICLAYLMKKRVRLBEAFEFVKORR 314
QY 448 FIARPPGFRLQIYQGIITASRQSHVWEQKGVSPPEHPAPEVSTPFPPL 500
DB 315 SIFSFMQQLQFESQVLT-----SCAEASPSGSL 350

RESULT 9

T46405
hypothetical protein DKFZp43401321.1 - human

C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 21-Jun-2002

C:Accession: T46405
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000

A:Reference number: 223034

A:Accession: T46405

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-303 <AAA>

A:Cross-references: EMBL:AL137704

A:Experimental source: adult testis; clone DKFZp43401321

A:Genetics:

A>Note: DKFZp43401321.1

Query Match 6.0%; Score 204.5; DB 2; Length 303;
Best Local Similarity 30.2%; Pred. No. 6.8e-06;
Matches 51; Conservative 30; Mismatches 71; Indels 17; Gaps 1;
332 IFPHLYLGSEWNAANLELORNRVTHILNMAREIDNFPYPERFYHNVRLWDESAQLPH 391
DB 108 ILPFLYLGSAVYAAARMDLALGITALLNVSDCPNHPGHYQKCIPEVDHNRADISSW 167
QY 392 WKETRRFEAARQGTIVLVHCKMGVSRSATVLAAMKQYECSEQLRHVOELRPIAR 451
DB 168 FMEAIEXYIDAVKCRGVLVHCOAGISRSATICLAYLMKKRVRLBEAFEFVKORRSTIS 227
QY 452 PNPGLFRLQIYQGIITASRQSHVWEQKGVSPPEHPAPEVSTPFPPL 500
DB 228 PNFSPMQLQFESQVLT-----SCAEASPSGSL 259

RESULT 10

A57126
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human

N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activate
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999

C:Accession: A57126

R:Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Keil
Science 259, 1763-1766, 1993

A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.

A:Reference number: A57126; PMID:93206122; PMID:7681221

A:Accession: A57126

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-314 <ROH>

A:Cross-references: GB:U11329; NID:G559539; PIDN:AAA50779.1; PID:G292376

C:Genetics:

A:Gene: GDB:DUSP2

A:Cross-references: GDB:139200

A:Map position: 2q11-2q11

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, an
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase

F:140-160/Region: nuclear location signal

F:189-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

F:251/Active site: Cys (phosphocysteine intermediate) #status predicted

F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 5.3%; Score 202; DB 1; Length 314;
Best Local Similarity 33.3%; Pred. No. 1e-05;
Matches 43; Conservative 31; Mismatches 55; Indels 0; Gaps 0;
332 IFPHLYLGSEWNAANLELORNRVTHILNMAREIDNFPYPERFYHNVRLWDESAQLPH 391
DB 176 ILPFLYLGSAVYAAARMDLALGITALLNVSDCPNHPGHYQKCIPEVDHNRADISSW 235
QY 392 WKETRRFEAARQGTIVLVHCKMGVSRSATVLAAMKQYECSEQLRHVOELRPIAR 451
DB 236 FQEAIGFDWVKNSSGGRVLVHCOAGISRSATICLAYLMKKRVRLBEAFEFVKORRGSVS 295
QY 452 PNPGLFRLQIYQGIITASRQSHVWEQKGVSPPEHPAPEVSTPFPPL 500
DB 296 PNFSPMQLQFESQVLT-----SCAEASPSGSL 304

RESULT 11

S29090
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human

N:Alternate names: protein-tyrosine-phosphatase C1100; protein-tyrosine-phosphatase, non

C:Species: Homo sapiens (man)

C:Date: 25-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999

A:Accession: S29090

R:Keyse, S.M.; Emslie, E.A.

Nature 359, 644-647, 1992

A:Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyrosine

A:Reference number: S29090; MUID:93024952; PMID:11406996

A:Accession: S29090

A:Molecule type: mRNA

A:Residues: 1-367 <KEY>

A:Cross-references: EMBL:X68277; NID:G29980; PIDN:CAA48338.1; PID:G29981

R:Kwak, S.P.; Hakes, D.U.; Martelli, K.J.; Dixon, J.E.

J. Biol. Chem. 269, 3596-3604, 1994

A:Title: Isolation and characterization of a human dual specificity protein-tyrosine pho

A:Reference number: A53052; MUID:94148864; PMID:8106404

A:Accession: A53052

A:Molecule type: DNA

A:Residues: 1-367 <KMA>

A:Experimental source: leukocyte

A>Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804

C:Genetics:

A:Gene: GDB:DUSP1; PTN10

A:Cross-references: GDB:136197; OMIM:600714

A:Map position: 5q34-5q34

C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
C:Keywords: heat shock; phosphoprotein; phosphoric monoester hydrolase; stress-induced
F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 5.8%; Score 202; DB 1; Length 367;
 Best Local Similarity 31.2%; Pred. No. 1.3e-05;
 Matches 43; Conservative 30; Mismatches 65; Indels 0; Gaps 0;

QY 332 IPFHLVGSWMNANLEIQRNVTIILNNAEIDNFERFYHNVRLWDESSAQLLH 391
 177 ILFLVIGSAYHSRCDMDALGITALINVSANCPHFECHYKSIPEVDNKKADISGW 236
 QY 392 WKETHRIEAPAAQGTHTLVHCKMGVSRSAATVLAAMQYECSLDQALRHVQELRPIAR 451
 237 FNEAIDFIDSIKNAQGRVVFHVCQAGISRSATICTLAVIMRTNRVXLDFAEFVQORSIIS 296
 QY 452 PNPGLRQIQYGGILTA 469
 297 PNPFGQLQFESQVLA 314
 DB

RESULT 12
 149365
 protein tyrosine phosphatase - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I49365
 R:Wistart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
 J. Biol. Chem. 270, 26782-26785, 1995
 A:Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-
 A:Reference number: I49364; MUID:96070766; PMID:7592316
 A:Accession: I49365
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-223 <RES>
 A:Cross-references: EMBL:U34973; NID:g1063624; PIDN:AAA7037.1; PID:g1063626
 C:Genetics:
 A:introns: 168/3
 C:Superfamily: VHL-type dual specificity phosphoprotein phosphatase homology
 F136-174/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 5.8%; Score 196.5; DB 2; Length 223;
 Best Local Similarity 33.8%; Pred. No. 1.4e-05;
 Matches 51; Conservative 27; Mismatches 66; Indels 7; Gaps 3;

QY 326 RRRASIFPHLYLGSWMN--ANLEBLQNRVTIILNNAEID-NF---YERFTYHNV 378
 26 REMOEVLPLGLPGYSSAMKSKLPLIQKGIITHICRONIEANFIKPNFQQLFRYLVL 85
 QY 379 RLWDESSAQLLPHWKETHRIEAPAAQGTHTLVHCKMGVSRSAATVLAAMQYECSLDQ 438
 86 DIADNPVENITIRFFPMTKETFDIGSLONGSKVLVHGNAGISRSAAAFVIAVIMETFGMKYRD 145
 DB 439 ALRHVQELRPIARPNPGLRQIQYGGILTA 469
 146 AFAYVOERFRCINPNAGFVHQEYEAITYLA 176
 QY

RESULT 13
 732494
 hypothetical protein COSB10.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32494
 R:Geisels, C.; Wamsley, P.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid COSB10.
 A:Reference number: Z21178
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-365 <GEN>
 A:Cross-references: EMBL:AF036685; PIDN:AA88308.1; GSPDB:GN00022; CESP:CO5B10.1
 A:Experimental source: strain Bristol N2; clone COSB10
 C:Genetics:
 A:Gene: CESP:CO5B10.1
 A:Map position: 4

A:introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2

Query Match 5.7%; Score 194.5; DB 2; Length 365;
 Best Local Similarity 26.5%; Pred. No. 3.9e-05;
 Matches 75; Conservative 32; Mismatches 113; Indels 63; Gaps 9;

QY 233 QERLNSSEOSCINENTAMADELSLRPPSAE----FGSSSEQEQMCAIRAEIMKYLVDVSDL 288
 54 QRLIMGSGMRSLSTVPDLKDLNNSPDQCEVLLIFGDSFQDQLSAAIARNL----- 104
 QY 289 ESVYSKEIRQLLELRGLP-----LQY---RDFID----- 316
 105 ---KSNHYRHFV---LGEPPVKTLLSQPFLTRDADENKNTTFQNNSPGASGQASSGP 158
 QY 317 ---NQMLLVAQRDRASRI-FP-----HLVGSWMNANLEIQRNVTIILNNAEID 366
 159 LNLNLQRLLEGEDQGRAPFPVKLTNFLVIGNAEFAKORNDVLKYSISHVIVTSLP 218
 QY 367 NFPEE--RFTYHNVRLWDESSAQLLPHWKETHRIEAPAAQGTHTLVHCKMGVSRSAATV 424
 219 NTFEEDPNMRYLRISADDNASHNLTKFPEAISFIDARRNDSACLHCLAGISRSVTIC 278
 QY 425 LAYAMQYECSLDQALRHVQELRPIARPNPGLRQIQYGGIL 467
 279 LAYIMKTEMCTLDSAYEWMQGNASINAPNPFMQQLDIYEMNL 321
 DB

RESULT 14
 S24411
 dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - mouse
 N:Alternate names: 3CH13 protein; protein-tyrosine-phosphatase erp, nonreceptor type 10
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
 C:Accession: A54681; S24411
 R:Noguchi, T.; Metz, R.; Chen, L.; Mattei, M.G.; Carrasco, D.; Bravo, R.
 Mol. Cell. Biol. 13, 5195-5205, 1993
 A:Title: Structure, mapping, and expression of erp, a growth factor-inducible gene encod
 A:Reference number: A54681; MUID:9336956; PMID:8355678
 A:Accession: A54681
 A:Molecule type: DNA
 A:Residues: 1-367 <NOG>
 A:Cross-references: GB:S64851; NID:g409976; PIDN:AA27882.1; PID:g409977
 R:Charles, C.H.; Abler, A.S.; Lau, L.F.
 Oncogene 7, 187-190, 1992
 A:Title: cDNA sequence of a growth factor-inducible immediate early gene and characteriz
 A:Reference number: S24411; MUID:92158357; PMID:1741163
 A:Accession: S24411
 A:Molecule type: mRNA
 A:Residues: 1-367 <CHA>
 A:Cross-references: EMBL:X61940; NID:g49735; PIDN:CAA43944.1; PID:g49736
 C:Genetics:
 A:Gene: erp
 A:introns: 123/1; 172/1; 245/1
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
 C:Keywords: immediate-early protein; phosphoprotein; phosphoric monoester hydrolase
 F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:258/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 5.7%; Score 194; DB 1; Length 367;
 Best Local Similarity 30.4%; Pred. No. 4.2e-05;
 Matches 42; Conservative 30; Mismatches 66; Indels 0; Gaps 0;

QY 332 IPFHLVGSWMNANLEIQRNVTIILNNAEIDNFERFYHNVRLWDESSAQLLH 391
 177 ILFLVIGSAYHSRCDMDALGITALINVSANCPHFECHYKSIPEVDNKKADISGW 236
 QY 392 WKETHRIEAPAAQGTHTLVHCKMGVSRSAATVLAAMQYECSLDQALRHVQELRPIAR 451
 237 FNEAIDFIDSIKNAQGRVVFHVCQAGISRSATICTLAVIMRTNRVXLDFAEFVQORSIIS 296
 QY 452 PNPGLRQIQYGGILTA 469
 297 PNPFGQLQFESQVLA 314
 DB

Db 297 PNFSGQLLOFESQVLA 314

RESULT 15

S52265

dual specificity phosphatase (EC 3.1.3.-) 1 - rat

M.Alternate names: protein-tyrosine-phosphatase Ctl00; protein-tyrosine-phosphatase, non

C.Species: Rattus norvegicus (Norway rat)

C.Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999

C.Accession: S52265

R.Muda, M.; Schlegel, W.; Arkinstall, S.

submitted to the EMBL Data Library, January 1995

A.Description: Pathways regulating Ctl00 gene expression in pituitary cells.

A.Reference number: S52265

A.Accession: S52265

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-367 <MUD>

A.Cross-references: EMBL:X84004; NID:9642264; PID:CAA58828.1; PID:9642265

C.Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity

C.Keywords: phosphoprotein; phosphoric monoester hydrolase

F.181-312/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>

F.258/Active site: Cys (phosphocysteine intermediate) #status predicted

F.264/Binding site: substrate phosphate (Arg) #status predicted

Query Match

5.7%; Score 194; DB 2; Length 367;

Best Local Similarity 30.4%; Pred. No. 4.2e-05;

Matches 42; Conservative 30; Mismatches 66; Indels 0; Gaps 0;

```

QY 332 IFPHLYGSEWNANLEELQNRVTHILNNAREIDNPERFTYHNVRLEDESQQLPH 391
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 177 ILSFLYLGSAYHARXMDLALGITALINVSANGCNHFEHGYKSIPEVDNKKADISSW 236
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 392 WKETHRFTEAPAGQGHVLYHCKGVSRSATVLYAMKQYEGSEQALRHVQELRPIAR 451
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 FNEAIDPIDISKAGGRVFWCOAGISRSATICLAYIMRTNRYKLDFAFEFYKRRSITS 296
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 452 PNPGLROLOIYQGIITA 469
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 297 PNFSGQLLOFESQVLA 314
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

Search completed: January 15, 2004, 06:50:27
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 15, 2004, 06:41:46 ; Search time 18 Seconds

(without alignments)
1721.700 Million cell updates/sec

Title: US-09-955-732-2

Perfect score: 3412
Sequence: 1 MALVTVSRSPFGSGASTPVG.....RRKRVQASVHDSGEGGEA 659

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 260 | 7.6 | 625 | 1 DUS6_HUMAN | Q13202 homo sapien |
| 2 | 254 | 7.4 | 217 | 1 DUS3_HUMAN | Q8W122 homo sapien |
| 3 | 253.5 | 7.4 | 665 | 1 DUSG_HUMAN | Q9BY84 homo sapien |
| 4 | 252 | 7.4 | 663 | 1 DUS8_MOUSE | Q09112 mus musculu |
| 5 | 239.5 | 7.0 | 482 | 1 DUS6_HUMAN | Q9Y6W6 homo sapien |
| 6 | 233 | 6.8 | 384 | 1 DUS5_RAT | Q54838 rattus norv |
| 7 | 232.5 | 6.8 | 483 | 1 DUS4_MOUSE | Q9A580 mus musculu |
| 8 | 229 | 6.7 | 295 | 1 DUS7_HUMAN | Q9H122 homo sapien |
| 9 | 226.5 | 6.6 | 320 | 1 DUS7_MOUSE | Q91246 mus musculu |
| 10 | 225.5 | 6.6 | 384 | 1 DUS9_HUMAN | Q9Y956 homo sapien |
| 11 | 224 | 6.6 | 384 | 1 DUS5_HUMAN | Q16690 homo sapien |
| 12 | 223.5 | 6.6 | 280 | 1 DUS7_RAT | Q61340 rattus norv |
| 13 | 217.5 | 6.3 | 320 | 1 DUS7_HUMAN | Q16829 homo sapien |
| 14 | 215.5 | 6.3 | 395 | 1 DUS4_RAT | Q62767 rattus norv |
| 15 | 210.5 | 6.2 | 619 | 1 VHPI_CAEEL | Q10038 caenorhabdi |
| 16 | 209 | 6.1 | 318 | 1 DUS2_MOUSE | Q05922 mus musculu |
| 17 | 205.5 | 6.0 | 394 | 1 DUS4_HUMAN | Q13115 homo sapien |
| 18 | 204 | 6.0 | 375 | 1 DUS4_CHICK | Q9PW71 gallus gall |
| 19 | 202 | 5.9 | 314 | 1 DUS2_HUMAN | Q05923 homo sapien |
| 20 | 202 | 5.9 | 367 | 1 DUS1_HUMAN | Q28632 mus musculu |
| 21 | 198.5 | 5.8 | 223 | 1 STYX_MOUSE | Q60969 mus musculu |
| 22 | 196.5 | 5.8 | 223 | 1 DUS1_MOUSE | Q64623 rattus norv |
| 23 | 194 | 5.7 | 367 | 1 DUS1_RAT | Q38690 saccharomyc |
| 24 | 194 | 5.7 | 489 | 1 MS6_YEAST | Q9461 mus musculu |
| 25 | 193 | 5.6 | 381 | 1 DUS6_MOUSE | Q9U16 homo sapien |
| 26 | 192.5 | 5.6 | 340 | 1 DUSC_HUMAN | Q9U16 homo sapien |
| 27 | 191.5 | 5.6 | 340 | 1 DUSC_HUMAN | Q9U16 homo sapien |
| 28 | 191 | 5.6 | 188 | 1 DUS7_HUMAN | Q9U16 homo sapien |
| 29 | 191 | 5.6 | 188 | 1 DUS7_HUMAN | Q9U16 homo sapien |
| 30 | 189.5 | 5.6 | 198 | 1 DUSD_HUMAN | Q9U16 homo sapien |
| 31 | 189.5 | 5.6 | 381 | 1 DUS6_RAT | Q9U16 homo sapien |
| 32 | 186.5 | 5.5 | 185 | 1 DUS3_HUMAN | Q9U16 homo sapien |
| 33 | 186.5 | 5.5 | 381 | 1 DUS6_HUMAN | Q9U16 homo sapien |

| | | | | | |
|----|-------|-----|------|--------------|--------------------|
| 34 | 184.5 | 5.4 | 198 | 1 DUSE_MOUSE | Q9117 mus musculu |
| 35 | 182.5 | 5.3 | 198 | 1 DUSE_HUMAN | Q9117 mus musculu |
| 36 | 181.5 | 5.3 | 125 | 1 DUSF_MOUSE | Q8142 mus musculu |
| 37 | 179.5 | 5.3 | 185 | 1 DUS3_MOUSE | Q94743 mus musculu |
| 38 | 177.5 | 5.2 | 276 | 1 PT93_CHLEU | Q9491 chlamydomon |
| 39 | 177.5 | 5.2 | 339 | 1 DUSC_MOUSE | Q9402 mus musculu |
| 40 | 175.5 | 5.1 | 364 | 1 PVH1_YEAST | Q02256 saccharomyc |
| 41 | 154 | 4.5 | 282 | 1 Y042_CAEEL | Q34680 caenorhabdi |
| 42 | 147 | 4.3 | 912 | 1 A36D_DROME | Q9331 drosophila |
| 43 | 140.5 | 4.1 | 1805 | 1 NEST_RAT | Q21263 rattus norv |
| 44 | 131.5 | 3.9 | 598 | 1 CCBI_BOVIN | Q9M17 bos taurus |
| 45 | 131.5 | 3.9 | 807 | 1 YB9T_YEAST | Q38148 saccharomyc |

ALIGNMENTS

```

RESULT 1
DUS6_HUMAN
ID DUS6_HUMAN STANDARD; PRT; 625 AA.
AC Q13202;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
DE (Dual specificity protein phosphatase hvh-5).
DE DUSP8 OR VHS.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Fetal brain;
RX MEDLINE=96009533; PubMed=7561891;
RA Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
RT "hvh-5: a protein tyrosine phosphatase abundant in brain that
RT inactivates mitogen-activated protein kinase.";
RL J. Neurochem. 65:1823-1833(1995).
CC -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC SMILARITY).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
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CC -----
CC EMBL: U27193; AAA83151.1; -
CC HSSP: Q16828; IMKP.
CC Genew: HGNC:3074; DUSP8.
CC MIM: 602038; -
CC GO: GO:0005757; C:cytoplasm; TAS.
CC GO: GO:0004725; F:protein tyrosine phosphatase activity; TAS.
CC GO: GO:000188; P:inactivation of MAPK; TAS.
CC GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro: IPR001340; D8 phosphatase.
CC InterPro: IPR001763; Rhodanese-like.
CC InterPro: IPR003877; TYR_phosphatase.
CC Pfam: PF00782; DSPC; 1.
CC SMART: SM00195; DSPC; 1.
CC SMART: SM00450; RHOD; 1.

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DR PROSITE; PS00206; RHODANESSE 3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00504; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolyase; Nuclear protein.
 FT DOMAIN 23 138 RHODANESSE.
 FT DOMAIN 162 430 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 310 550 PRO-RICH.
 FT ACT_SITE 246 246 BY SIMILARITY.
 SQ SEQUENCE 625 AA; 65840 MW; DCEBAL1487219666 CRC64;
 Query Match 7.6%; Score 260; DB 1; Length 625;
 Best Local Similarity 30.8%; Pred. No. 1.2e-08;
 Matches 78; Conservative 36; Mismatches 113; Indels 26; Gaps 7;
 QY 330 SRFFPLLYGSEWMAANLEELQNRVTHILNMAARE---DNYPFRFTYHNRWLMDDESA 386
 DB 162 TRLPFLYLGSDVDVANKDMLTONGISVYLNASNSCPKDFICESEFM--RPVIDNACE 219
 QY 387 QLLPHKETHRFTLEAARAGTHTLVHCKWGSRSATVLAAMKOYECSLBOALRHVOEL 446
 DB 220 KLLPMLDKIEFLIDKAKSSCOYIVHCLAGISRSATIAIAYIMKMGSSDDAYAFVDR 279
 QY 447 RPIAPNPGFLRLOLIYGI--LTASRGHWKQYGVSPENHAPVSTPPL-PPH 503
 DB 280 RPSISNPFNLGQLLEYERTLKLALQG--DPTSGTPEPPSPAPAGLPLPLPPT 336
 QY 504 PEGCGSEKTVGMEESQAPKEEGPPR-----RINLRGVRSLILEP-----SL 548
 DB 337 SEEAALGNAAARBGISAGCEPPAPPTPATSAQGLRGLHLSLSDRLQDTNRLKRSPSL 396
 QY 549 ELESTSTSDMPE 561
 DB 397 DIKSAVAPSRRPD 409
 RESULT 2
 ID DUSU_HUMAN STANDARD; PRT; 217 AA.
 AC O8WTR2; O8WYN4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-FEB-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 19 (EC 3.1.3.48) (Protein phosphatase SKRP1).
 GN DUSP19 OR DUSP17.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Zama T., Aoki R., Kamamoto T., Inoue K., Ikeda Y., Hagiwara M.;
 RT "SKRP1, a novel member of dual-specificity phosphatase family and its scaffold role for JNK signalling pathway";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Kikuchi K., Nakamura K., Sato T., Shima H.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Griese L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Srapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Tsien T.B., Toshiyuki S., Carninci P., Piatte S.J.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Molligh S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc Natl Acad Sci U S A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=O8WTR2-1; Sequence=Displayed;
 CC Name=2; Synonyms=short;
 CC IsoId=O8WTR2-2; Sequence=VSP_005138;
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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 CC EMBL; AB063186; BAB83498.1; -;
 CC EMBL; AB063187; BAB83499.1; -;
 CC EMBL; AB038770; BAB82499.1; -;
 CC EMBL; BC035000; AAH35000.1; -;
 CC HSSP; Q16828; IMKP.
 CC GeneW; HGNC:18894; DUSP19.
 CC InterPro; IPR000340; DS_phosphatase.
 CC InterPro; IPR000387; TYR_phosphatase.
 CC Pfam; PF00782; DSPC; 1.
 CC SMART; SM00185; DSEF; 1.
 CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE NEG.
 CC DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
 CC DR PROSITE; PS00504; TYR_PHOSPHATASE_DUAL; 1.
 CC KW Hydrolyase; Alternative splicing.
 CC FT DOMAIN 133 197 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 150 150 BY SIMILARITY.
 CC FT VARSPLIT 91 141 Missing (in isoform 2).
 CC SQ SEQUENCE 217 AA; 24194 MW; A9FAB082D35EC442 CRC64;
 Query Match 7.4%; Score 254; DB 1; Length 217;
 Best Local Similarity 40.6%; Pred. No. 6.7e-09;
 Matches 54; Conservative 25; Mismatches 54; Indels 0; Gaps 0;
 QY 332 IFPLLYGSEWMAANLEELQNRVTHILNMAAREINDPFRFTYHNRWLMDDESAQLRPH 391
 DB 69 IKPMLLGSDAAHDLTLKKNKVTHTLVNVAAGVNAFLSDFTYKSSIDLDPELTILSY 128
 QY 392 WKETHRFTLEAARAGTHTLVHCKWGSRSATVLAAMKOYECSLBOALRHVOELRPIAR 451
 DB 129 FPECFEFTLEAKKRGDGVVLAHCAVSRRAAIYIGFLMSSEQTSFSAFSLVKNRPSIC 188
 QY 452 PNPGLRLOLIYQ 464
 DB 189 PNSGFMEQLRTRYQ 201
 RESULT 3
 ID DUSG_HUMAN STANDARD; PRT; 665 AA.
 AC O9BY84; O9C0G3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 16 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Mitogen-activated protein kinase phosphatase 7) (MAP kinase
 DE phosphatase 7) (MKP-7).
 GN DUSP16 OR MKP7 OR KIAA1700.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21486429; PubMed=11489891;
 RA Masuda K., Shima H., Watanabe M., Kikuchi K.;
 RT "MKP-7, a novel mitogen-activated protein kinase phosphatase,
 RT functions as a shuttle protein."
 RL J. Biol. Chem. 276:39002-39011(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21082932; PubMed=11214970;
 RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 7:347-355(2000).
 CC -1- FUNCTION: Involved in the inactivation of MAP kinases.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC -----
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 CC -----
 CC DR EMBL; AB052156; BAB40814.1; -
 CC DR EMBL; AB051487; BAB21791.1; ALT_INIT.
 CC DR HSSP; Q16828; IMKP.
 CC DR Genew; HGNC:17909; DUSP16.
 CC DR MIM; 607175; -
 CC DR GO; GO:0005737; Cytoplasm; TAS.
 CC DR GO; GO:0005634; C:nucleus; TAS.
 CC DR GO; GO:0000188; P:inactivation of MAPK; TAS.
 CC DR GO; GO:0045209; P:leptotyrosin B-sensitive MAPK phosphatase nuc. .; TAS.
 CC DR GO; GO:0045204; P:MAPK nucleus export; TAS.
 CC DR InterPro; IPR000340; DS_phosphatase.
 CC DR InterPro; IPR001763; Rhodanese-like.
 CC DR InterPro; IPR000387; Tyr_phosphatase.
 CC DR Pfam; PF00782; DSPC; 1.
 CC DR Pfam; PF00581; Rhodanese; 1.
 CC DR SMART; SM00195; DSPC; 1.
 CC DR SMART; SM00450; RHOD; 1.
 CC DR PROSITE; PS00206; RHODANES_3; 1.
 CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 CC DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 CC DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 CC KM Hydroxylase/ Nucleic protein.
 CC FT DOMAIN 22 137 RHODANES.
 CC FT DOMAIN 227 289 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 244 244 BY SIMILARITY.
 CC SQ SEQUENCE 665 AA; 73101 MW; 1B853FF08460DF CAC64;

QY 330 SRIFPHYLIGSEWNAANIELQNRVTHILNMAREI--DNFYPERFYHNVRLMDEESAQ 387
 Db 160 TRILPNLYLGQGRVUNKEMLQNGIGIVYLANSTCKPKPIFESH-FLAVPNDSCCK 218
 QY 388 LLPHWKETHRFIEAARQGHVLYHNCMGVSRSAATVLAAMQYEGSLQALRHVOELR 447
 Db 219 ILPLWLDKSVDFIEKAKSNOCVLYHCLAGISRSATVIAIAYIMKMDMSLDEAYRFVKEKR 278
 QY 448 PIARPNPGFLRQLOIYQGIILTASRSHWEQKGVAPSEHPAPE-----VSTFPPLPP 502
 Db 279 FTISNNFLIGQLDY-----EKTKNQGASGPKSKLTLHLERNEVPA 325
 QY 503 EPEGGGG-EXYVGEESQAAPKEPPRPIN-----LKGVM 538
 Db 326 VSEGGQKSETPPLSPCCDSATSENAQRP-VHPASVSPSVQPSLLEDSPLYQALSLGLH 384
 QY 539 RSISLEP-----SLEESTSESDMP---EVFSHSHSE 571
 Db 385 LSAPRLSDSNKLRKPSFLDIKSVSYSAKVAASLHGFSSEDALE 428
 RESULT 4
 DUSP_MOUSE
 ID DUSP_MOUSE STANDARD; PRT; 663 AA.
 AC 009112;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Neuronal tyrosine threonine phosphatase 1).
 GN DUSP8 OR NTRP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=66311565; PubMed=8733137;
 RA Theodosiou A.M., Rodriguez N.R., Nesbitt M.A., Ambrose H.J.,
 RA Paterson H., McCellan-Arnold E., Boyd Y., Leversha M.A., Owen N.,
 RA Blake D.J., Ashworth A., Davies K.E.;
 RT "A member of the MAP kinase phosphatase gene family in mouse
 RT containing a complex trinucleotide repeat in the coding region."
 RL Hum. Mol. Genet. 5:675-684(1996).
 CC -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN AND LUNG.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC -----
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 CC -----
 CC EMBL; X95518; CAA64772.1; -
 CC HSSP; Q16828; IMKP.
 CC DR MGD; MGI:106626; Dusp8.
 CC DR InterPro; IPR000340; DS_phosphatase.
 CC DR InterPro; IPR001763; Rhodanese-like.
 CC DR InterPro; IPR000387; Tyr_phosphatase.

Query Match 7.4%; Score 253.5; DB 1; Length 665;
 Best Local Similarity 29.6%; Pred. No. 3.2e-08;
 Matches 84; Conservative 44; Mismatches 99; Indels 57; Gaps 9;


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QY 232 YQERLSEQSCINENTWAMADLSLRPSAEP-----CGSSEQOMQOAI---RAELMKYLD 284
DB 236 YDENTNPSRWVPSQPLHIVLSLKNRGEKPLVKGGLSPQCNHNHNDLSLQOECKE 295
QY 285 VSDLESVTSKEIRQALERLGLPLQOYRDFIDNOMLLVAORDRASRIFPHLYLSEWNA 344
DB 296 VGGAGAAASLLPQ-----PIPTPD-ENAEI-----TPILPFLFNEDQDA 337
QY 345 ANLEELQNRVTHILNAREIDNFPYER--FTYHNVRLMDESAQLPMPKXTHFTEARA 402
DB 338 QDDLTWQRLNIGVIVNVTTHLPVHYEKLFPYKRLPATDSNKNLROQYFEZAFEFIEEA 397
QY 403 RAQGTIVLVHCKKGVSRSAATVLAAYAMKQYECSLQALRHVOELSPARPNPGFLROLQI 462
DB 398 HCGGKGLLHCGAGVSRSAITIVAYIMKRTMTMDAYKVGKRPILSPNLFNGQLLE 457
QY 463 YQGITLTSRQSHVWEQKGV 483
DB 458 FEEDLNGVTPRILTPKLMGV 478

RESULT 6
DUS5_RAT
ID DUS5_RAT STANDARD: PRT; 384 AA.
AC 054838;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16)
(MAP-kinase phosphatase Cpg21).
DUSP5.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar;
RX MEDLINE=98364306; PubMed=9699150;
RA Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A.,
RA Mangelus M., Silverman M.A., Kedat H., Naor C., Korman M., Hancock T.,
RA Seger R., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.,
RT "Hippocampal plasticity involves extensive gene induction and multiple
RT cellular mechanisms."
RL J. Mol. Neurosci. 10:75-98(1998).
CC -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -1- SIMILARITY: Contains 1 rhodanase domain.
CC
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CC
CC EMBL: AF013144; AAB94858.1; -.
CC HSSP: Q16828; 1MKP.
CC InterPro: IPR000340; DS_phosphatase.
CC InterPro: IPR001763; Rhodanase-like.
CC InterPro: IPR000387; TYR_phosphatase.
CC Pfam: PF00782; DSPC; 1.
CC Pfam: PF00581; Rhodanase; 1.
CC SMART: SM00195; DSPC; 1.

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DR SMART: SM00450; RHOD: 1.
DR PROSITE; PS50206; RHODANASE_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Nuclear protein.
FT DOMAIN 19 141 RHODANASE.
FT DOMAIN 180 384 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 53 74 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ACT_SITE 79 82 POLY-GLY.
FT ACT_SITE 263 263 BY SIMILARITY.
SQ SEQUENCE 384 AA; 42094 MW; 56440698BD48700 CRC64;

Query March 6.8%; Score 233; DB 1; Length 384;
Best local similarity 31.2%; Pred. No. 2.7e-07;
Matches 67; Conservative 30; Mismatches 84; Indels 34; Gaps 5;

QY 291 VTSKEIRO-ALERLGLPLQOYRDFIDNOMLLVAQR---DRAS--RIFPHLYLSEWNA 344
DB 141 VDAPKPISEKLEGERGLSQ-----CGKPILSVAAYPAVDQGGPVELPFLVLSGAYHA 194
QY 345 ANLEELQNRVTHILNAREIDNFPYERFTYHNVRLMDESAQLPMPKXTHFTEARA 404
DB 195 SKCEFLNLHITALLNVSRTSEACTTHLYKXIPVDSHTADISGFQDAIDFCVRE 254
QY 405 QGTHVLVHCKKGVSRSAATVLAAYAMKQYECSLQALRHVOELSPARPNPGFLROLQIYQ 464
DB 255 ECGKVLVHCKAGVSRSTICMAYIMKQKRLKAEAFYIQRSSVSPNCGFQGLQY- 313
QY 465 GILTSRQSHVWEQKGVSPPEHPAEVSTPPPP 499
DB 314 -----EELIPSTPTPOPP 327

RESULT 7
DUS5_MOUSE
ID DUS5_MOUSE STANDARD: PRT; 483 AA.
AC Q9ES50; Q9CZY9;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dual specificity protein phosphatase 10 (EC 3.1.3.48) (EC 3.1.3.16)
(Mitogen-activated protein kinase phosphatase 5) (MAP kinase
DE phosphatase 5) (MKP-5).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=20515587; PubMed=11060451;
RA Masuda K., Shima H., Kikuchi K., Watanabe Y., Matsuda Y.,
RT "Expression and comparative chromosome mapping of MKP-5 genes
RT DUSP10/Dusp10."
RL Cytogenet. Cell Genet. 90:71-74(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischiemann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakurai L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Batsch G.,
RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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RA Villalón J.C., Muzny D.M., Sodergren E.J., Lu X.R., Gibbs S.A.,
RA Fahney U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC Name=2;
CC IsoId=G9HNR2-1; Sequence=Displayed;
CC IsoId=G9HNR2-2; Sequence=VSP_007292, VSP_007293;
CC Note=Derived from EST data;
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUPERFAMILY.
CC -1- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -1- CAUTION: Although assigned as two separate genes (c20orf57 and
CC DUSP1), it is probable that C20orf57 does not exist by itself and
CC is a part of the DUSP15 gene.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-stb.ch).
CC -----
DR EMBL AK0374430; BAC05048.1; --
DR EMBL AL160175; CACI0008.2; ALT_SEQ.
DR EMBL AL160175; CACC898.1; ALT_SEQ.
DR EMBL BM554314; -; NOT_ANNOTATED_CDS.
DR HSPP P51452; IYHR..
DR Genew; HGNC:16236; DUSP15.
DR Genew; HGNC:16190; C20orf57.
DR InterPro; IPRO00340; DS_phosphatase.
DR InterPro; IPRO00387; TYR_phosphatase.
DR Pfam; PF00782; DSPC_1.
DR SMART; SMO0195; DSPC_1.
DR PROSITE; PS00383; TYR_PHOSPATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPATASE_DUAL; 1.
KM Hydroxylase; Alternative splicing.
FT DOMAIN 62 132 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 85 85 BY SIMILARTY.
FT VARSPPLIC 143 232 GARSTKTSQAOCPMTSATCILAAVALTLAALVAREATG
FT FT RAAGSCRLPSAPLAERLLGPYPHAAGSPDKOICFG
FT FT EDDEGPTD -> LRGLEERRGGSPRREREILLPLCKR
FT FT CRGSGLATSASSAGPRSAASGEIVQNLVVTRTREARRLPPLL
FT FT ARVKQTISCLDPRLSKRKCGK (in isoform 2).
FT /ftid=vsp_007292.
FT Missing (in isoform 2).
FT /ftid=vsp_007293.
SQ SEQUENCE 295 AA; 31881 MW; 28F8A687ECB5C219 CRC64;
Query Match 6.7% Score 229; DB 1; Length 285;
Beet Local Similarity 27.2%; Fred No. 3.4e-07;
Matches 71; Conservative 39; Mismatches 119; Indels 32; Gaps 6;
Cy 332 IFPHYLISENNANALEELQNRVRVHLINMAREIDNPFPERFRVTYNVLMDSEAKOLPH 391
Db 5 VLPGLYGNFLDAKDLDLGKNKKITHISI-HESQPDLLODTITVIRIVALTPEVPICKH 63
Cy 392 WKETHRFLEARDAGCTHVLVHCNKGVSSAATLTAVAMKYQCSIEQLRHVQELRPJAR 451

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| | | | |
|----------|--|--|--------------|
| Db | 64 | FKECINFIHCRNLGNGLVCHFCFACISSTTIVAYVTVGLGRVDLLEAIKARPLAN | 123 |
| Qy | 452 | PNPGFLRQLVYQGLITLSRSHWEQKVGVSPEEH-----AEVSTPPPLPEPEG | 506 |
| Db | 124 | PNPGFRQDLLEFGVASSCKGARHRTSKTSGAQCPMTSATCULARVALLSAALVREATG | 183 |
| Qy | 507 | -----GGEKVKVMEESQA-----PK-----EEGPPPRINLRGWMASI | 541 |
| Db | 184 | RTAQRCSRSPAAAERLIGPPPHVAAGMSPPPKYQICLCFGEEDGPPQHPEQLIMADV | 243 |
| Qy | 542 | SL-LEPSLESTSETSDMPE | 561 |
| Db | 244 | QVQLRPGSSSCTLSATERPD | 264 |
| RESULT 9 | | | |
| ID | DUS7_MOUSE | STANDARD; | PRT; 320 AA. |
| AC | Q91246; | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | |
| DE | Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16). | | |
| GN | DUSP7. | | |
| OS | Mus musculus (Mouse). | | |
| CC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| CC | NCBI_TaxID=10090; | | |
| RP | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K., | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | |
| RA | Ditchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L., | | |
| RA | Stapleton W., Soares W.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | |
| RA | Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullany S.J., | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | |
| RA | Faney J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., | | |
| RA | Walling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | |
| RA | Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E., | | |
| RA | Schnecher A., Schein J.E., Jones S.J.M., Marra M.A.; | | |
| RT | "Generation and initial analysis of more than 15,000 full-length | | |
| RT | human and mouse cDNA sequences." | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002). | | |
| CC | -1- CATALYTIC ACTIVITY. Protein tyrosine phosphatase + H(2O) = protein | | |
| CC | tyrosine + phosphate. | | |
| CC | -1- CATALYTIC ACTIVITY. A phosphoprotein + H(2O) = a protein + | | |
| CC | phosphate. | | |
| CC | -1- SUBCELLULAR LOCATION. Cytoplasmic (By similarity). | | |
| CC | -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN- | | |
| CC | TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY. | | |
| CC | ----- | | |
| CC | THIS SWISS-PROT entry is copyright. It is produced through a collaboration | | |
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| CC | use by non-profit institutions as long as its content is in no way | | |
| CC | modified and this statement is not removed. Usage by and for commercial | | |
| CC | entities requires a license agreement (See http://www.isb.ch/announcement/ | | |
| CC | or send an email to license@isb-sib.ch). | | |
| CC | ----- | | |
| DR | EMBL; BC010207; AAH10207.1; - | | |
| DR | MED; MG1:2387100; Dusp7. | | |
| DR | InterPro; IPR000347; DS phosphatase. | | |
| DR | InterPro; IPR000387; Tyr_phosphatase. | | |
| DR | Pfam; PF00782; DSpC; 1. | | |

DR SMART, SM00195; DSPC, 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50052; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KM Hydrolyase.
 FT DOMAIN 209 277 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 232 232 BY SIMILARITY.
 FT SEQUENCE 320 AA; 35258 MW; 2AAD2723E27DAE53 CRC64;
 SQ
 Query Match 6.6%; Score 226.5; DB 1; Length 320;
 Best Local Similarity 25.0%; Pred. No. 5.3e-07;
 Matches 91; Conservative 43; Mismatches 117; Indels 113; Gaps 12;
 QY 152 PSSSSSCTGLVPLMSDTQYVLDG-----DGFSTVSGGQSRIFKPISTQVWATLQ 205
 DB 46 PEPGASVYGLLQKLRD-----DCCQAYVYGGFN-----KQITYS-- 84
 QY 206 VHQACEALGSLVPGSGALTWASHYQERLNSGSCINMTWAMDLSPPSAPGGS 265
 DB 85 -----EHCETVSDSSSPSGSP-----TSVGLGLRLISDCSDGE 121
 QY 266 SEEDQMEQALRAELMKVLDVSDLESTVSKETQALHLGLPLQGYRPFINDQMLLYAQ 325
 DB 122 SRELEPSSATB-----SDGSPVPSQ-----PAFVQ----- 148
 QY 326 RBRASRIFPHLYGSEMNANTLELQNRVTHILNMAEIDNFPYE--RTYHNVRIMDE 383
 DB 149 -----LPEYVLGCAKSDTNLDVCKYKIKILNTPPLPAFHGSEFTYKQIPISDH 202
 QY 384 ESAQLPHEKTHRTFTEARAQSTHYLVHCKMGVRSAAATVLAVMKQYEGLEQALNHV 443
 DB 203 WSNQLSQFPPEAISIFDEARSKKCGVLVHCLAGISRSVTVVAYVMOKNLSINDAYDFV 262
 QY 444 QELRPALRNPGRLQIQYGLITASRQSHWEOXGVSPDEHPAPE---VSTP--- 496
 DB 263 KRKXGISPVNFNGQLDF-----ERTLGSSCDNHAHSEQLYFTPTNNH 309
 QY 497 --FP 498
 DB 310 NLEP 313
 RESULT 10
 DUS9 HUMAN STANDARD; PRT; 384 AA.
 ID DUS9 HUMAN STANDARD; PRT; 384 AA.
 AC 099956;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 9 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Mitogen-activated protein kinase phosphatase 4) (MAP kinase
 DE phosphatase 4) (MKP-4).
 GN DUSP9 OR MKP4.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97184169; PubMed=9030581;
 RA Mada M., Boscher U., Smith A., Antonson B., Gallieron C.,
 RA Chabert C., Camps M., Martinou I., Ashworth A., Arkinstall S.,
 RT Molecular cloning and functional characterization of a novel
 RT mitogen-activated protein kinase phosphatase, MKP-4.";
 RL J. Biol. Chem. 272:5141-5151(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Platterer M.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INACTIVATES MAP KINASES. HAS A SPECIFICITY FOR THE ERK
 CC FAMILY.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein

CC tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Y08302; CA69610.1; -.
 DR EMBL; U52111; -, NOT_ANNOTATED_CDS.
 DR HSP; Q16828; MKP.
 DR Genew; HGNC:3076; DUSP9.
 DR MIM; 300134; -.
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0000188; P:inactivation of MAPK; TAS.
 DR GO; GO:0007254; P:TNK cascade; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000340; D:phosphatase.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANSE_3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50052; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KM Hydrolyase.
 FT DOMAIN 18 139 RHODANSE.
 FT ACT_SITE 203 384 PROTEIN-TYROSINE PHOSPHATASE.
 FT SEQUENCE 384 AA; 41867 MW; F8598CA95AB379B7 CRC64;
 SQ
 Query Match 6.6%; Score 225.5; DB 1; Length 384;
 Best Local Similarity 30.0%; Pred. No. 7.8e-07;
 Matches 68; Conservative 30; Mismatches 92; Indels 37; Gaps 5;
 QY 284 DVSDLESVTSKTRQA-----LEIRLGLPLQGYRPFINDQMLLYAQDASRI 332
 DB 170 DCSDAEADRDSDSCGIDSEGAAPPVGLRASFPVQ-----I 207
 QY 333 FPHLYGSEMNANTLELQNRVTHILNMAEIDNFPYE--RTYHNVRIMDEESAQLDF 390
 DB 208 LPNLYLSADSDAVLSLALGIRYILNTPPLNPFPEKQGDHYKQIPISDIWSQNLKR 267
 QY 391 HMKETHRTFTEARAQSTHYLVHCKMGVRSAAATVLAVMKQYEGLEQALNHVQELRP 450
 DB 268 FFPALIFIDELALSQNGVLVHCLAGISRSVTVVAYVMOKNLSINDAYDKRKXSN 327
 QY 451 RPNPGLRQIQYGLITASRQSHWEOXGVSPDEHPAPEVSTP 496
 DB 328 SPNPFNGQLDFERSLRT-EERHSQSGGSGGASASNPSPFTTP 373
 RESULT 11
 DUS5 HUMAN STANDARD; PRT; 384 AA.
 ID DUS5 HUMAN STANDARD; PRT; 384 AA.
 AC Q16930; Q12997;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase hvh3).
 GN DUSP5 OR VH3.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95138103; PubMed=7836374;
 RA Kwak S.P., Dixon J.E.;
 RT Multiple dual specificity protein tyrosine phosphatases are
 expressed and regulated differentially in liver cell lines.";
 RT J. Biol. Chem. 270:1156-1160(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=95050849; PubMed=7961985;
 RA Ishibashi T., Bottaro D.P., Michiel P., Kelley C.A.,
 RA Aaronson S.A.;
 RT "A novel dual specificity phosphatase induced by serum stimulation
 and heat shock.";
 RT J. Biol. Chem. 269:29897-29902(1994).
 RN [3]
 RP REVISIONS.
 RA Bottaro D.P.;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DISPLAYS PHOSPHATASE ACTIVITY TOWARD SEVERAL SUBSTRATES.
 CC THE HIGHEST RELATIVE ACTIVITY IS TOWARD ERK1.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 phosphate.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 rhodanese domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U16996; AAB06261.1; -;
 DR EMBL; U15932; AAG4693.2; -;
 DR HSSP; Q16828; IMKP.
 DR GeneW; HGNC:3071; DUSP5.
 DR MIM; 603069; -;
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR Pfam; PF00581; Rhodanese; 1.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS50206; RHODANSE_3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KM Hydrolyase; Nuclear protein.
 FT DOMAIN 180 141
 FT DOMAIN 180 384
 FT DOMAIN 53 74
 FT DOMAIN 79 82
 FT ACT_SITE 263 263
 FT CONFLICT 9 11
 FT CONFLICT 71 71
 FT CONFLICT 105 106
 SQ SEQUENCE 384 AA; 42107 MW; D2B726F7C041A306 CRC64;

Query Match 6.6%; Score 224; DB 1; Length 384;
 Best Local Similarity 27.7%; Pred. No. 9.6e-07;
 Matches 62; Conservative 40; Mismatches 84; Indels 38; Gaps 5;
 QY 287 DLESVTSKEI--RQALELRGLPL--QQYRDFIDNQMLLVAQDRASRIFFPHLYLQSEW 342
 DB 142 DVKPISEKIESEKESALLSQCGKPVVNSYRPAYD-----QCGVEILPFLYLSAY 192
 QY 343 NAAVLESELRNRVTHLMAREIDNFFPERFTYNNVRLMPEBSAQLLPHMKETHRIEAA 402
 DB 193 HASCEFLANDLHITALLNVSRRSEACMTHLHYKMFVEEDSHDADISSHQEALDFIDCV 252
 QY 403 RAQGHVLYVHCQGVSSAAATVLAAYAKQYECSEALRHYOELRPAPRNPGLPOLQI 462
 DB 253 REKGRVLYVHCAGISSPTICMAYLMKTFQFLKAEFDYIKQRRSVNSNFGMQLLQ 312
 QY 463 YQGITLARSQSHVNEQKVGVSPEHPAPVSTPFPPLPEPEG 506
 DB 313 YESEILP-----STP-NQPPSCQ 331
 RESULT 12
 DUST_RAT
 ID DUST_RAT STANDARD; PRT; 280 AA.
 AC Q63340;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase MKP-X) (Fragment).
 GN DUSP7 OR MKPX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Neuron;
 RX MEDLINE=96224012; PubMed=8626780;
 RA Camps M., Boscher U., Dickinson R., Martinou J.C., Martinou I.,
 RA "MKP-3, a novel cytosolic protein-tyrosine phosphatase that
 exemplifies a new class of mitogen-activated protein kinase
 phosphatase.";
 RT J. Biol. Chem. 271:4319-4326(1996).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 tyrosine + phosphate
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X94186; CA63896.1; -;
 DR HSSP; Q16828; IMKP.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KM Hydrolyase.
 FT NON_TER 1 1

FT DOMAIN 169 237 PROTEIN-TYROSINE PHOSPHATASE.
 ACT_SITE 192 192 BY SIMILARITY
 SQ SEQUENCE 280 AA; 30666 MW; 45DEF49222BDDF CRC64;
 Query Match 6.6%; Score 223.5; DB 1; Length 280;
 Best Local Similarity 24.3%; Pred. No. 6,8e-07;
 Matches 86; Conservative 47; Mismatches 128; Indels 93; Gaps 10;

QY 152 PDSSSSCTGLVLPMSDQVYLDG-----DGGFSVTSGGQSRIEKRISIQTMWATLQ 205
 DB 6 PEPGAPASVGLLQKLRD-----DGCQAYYLOGGFN-----KQTEYS--- 44
 QY 206 VHQACEAALGSLVPGSGALTWASHYQERLNSGSCINMTAMADELSRPSAEPGGS 265
 DB 45 ---EHETNVDSSSSSP-----TSVGLGGRISDSCDGE 81
 QY 266 SEQOWEQAIRAEIMKVLVDLSVTSKEIRQALERLGLPQQYRFDINDOMLLVQAQ 325
 DB 82 SDRLEPSSATP-----SDGSPVPSGQ-----PAFVQ----- 108
 QY 326 RDRASRIFFPHLYGSENNANLELQNRVTHILNAREIDNFEPE--RTYHNYRLMDE 383
 DB 109 -----ILPYLYGCAKSDTNLDVGRGKIKYILNTPNLPNAPFEGEFTYKQIPISDH 162
 QY 384 ESAQLPWHKETHRFTEAARAGTHTVYHCKMGVSSAATVLAANKQYCSLEQALRHV 443
 DB 163 WSONLSGFPEPAISFIDEARSKKCGVLVHCLAGISRSVTVVAYLMQKNLSLNDAYDFV 222
 QY 444 QELRPAPNPFGFLRQLOIYQGITLNSR--QSHVMEQKVGVSPEEHPEVST 495
 DB 223 KRKKSNISSPNFNMWGLDPERTLGLSSPCDNHTSEQIYFSTPTNHLFPINT 276

RESULT 13
 DUST_HUMAN STANDARD; PRT; 320 AA.
 ID DUST_HUMAN
 AC Q16829;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase PYST2).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96312959; PubMed=8670865;
 RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.;
 RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pystl,
 RT a novel cytosolic dual-specificity phosphatase.";
 RL EMBO J. 15:3621-3632(1996).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X93921; CA66814.1; ALT_INIT.
 DR HSSP; Q16828; IMKP.

DR Genew; HGNC:3073; DUSP7.
 DR MIM; 602749; -.
 DR GO; GO:0005173; C:cytoplasm; ISS.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; ISS.
 DR GO; GO:0000188; P:inactivation of MAPK; ISS.
 DR InterPro; IPR00340; DS_phosphatase.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR Pfam; PF00782; DSGC; 1.
 DR SMART; SM00195; DSGC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 DR HydroLase.
 FT ACT_SITE 209 277
 FT DOMAIN 232 232
 FT ACT_SITE 232 232
 SQ SEQUENCE 320 AA; 35278 MW; D387F6BEFFBA9213C CRC64;

Query Match 6.4%; Score 217.5; DB 1; Length 320;
 Best Local Similarity 24.2%; Pred. No. 1.9e-06;
 Matches 84; Conservative 45; Mismatches 125; Indels 93; Gaps 10;

QY 152 PDSSPECTGLVLPMSDQVYLDG-----DGGFSVTSGGQSRIEKRISIQTMWATLQ 205
 DB 46 PEPGAPASVGLLQKLRD-----DGCQAYYLOGGFN-----KQTEYS--- 84
 QY 206 VHQACEAALGSLVPGSGALTWASHYQERLNSGSCINMTAMADELSRPSAEPGGS 265
 DB 85 ---EHETNVDSSSSSP-----TSVGLGGRISDSCDGE 121
 QY 266 SEQOWEQAIRAEIMKVLVDLSVTSKEIRQALERLGLPQQYRFDINDOMLLVQAQ 325
 DB 122 SDRLEPSSATP-----SDGSPVPSGQ-----PAFVQ----- 148
 QY 326 RDRASRIFFPHLYGSENNANLELQNRVTHILNAREIDNFEPE--RTYHNYRLMDE 383
 DB 149 -----ILPYLYGCAKSDTNLDVGRGKIKYILNTPNLPNAPFEGEFTYKQIPISDH 202
 QY 384 ESAQLPWHKETHRFTEAARAGTHTVYHCKMGVSSAATVLAANKQYCSLEQALRHV 443
 DB 203 WSONLSGFPEPAISFIDEARSKKCGVLVHCLAGISRSVTVVAYLMQKNLSLNDAYDFV 262
 QY 444 QELRPAPNPFGFLRQLOIYQGITLNSR--QSHVMEQKVGVSPEEH 488
 DB 263 KRKKSNISSPNFNMWGLDPERTLGLSSPCDNHSSQIYFSTPTN 309

RESULT 14
 DUS4_RAT STANDARD; PRT; 395 AA.
 ID DUS4_RAT
 AC Q62767;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Mitogen-activated protein kinase phosphatase-2) (MAP kinase
 DE phosphatase-2) (MKP-2).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=hepochromocytoma;
 RX MEDLINE=95301550; PubMed=7782322;
 RA Wiersma A., Kim C.S., Yao H., Roberson M.S., Stork P.J.S.;
 RT "A novel mitogen-activated protein kinase phosphatase. Structure,
 RT expression, and regulation.";
 RL J. Biol. Chem. 270:14587-14596(1995).
 CC -1- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
 CC DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
 CC ERK1 AND ERK2 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein

```
CC tyrosine + phosphate.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT MODERATE LEVELS IN NEARLY ALL
CC TISSUES AND CELLS INCLUDING BRAIN, SPLEEN, AND TESTES WITH THE
CC HIGHER EXPRESSION IN THE HEART AND LUNG AND LOWER EXPRESSION IN
CC SKELETAL MUSCLE AND KIDNEY. UNDETECTABLE IN LIVER. EXPRESSED IN
CC MANY AREAS OF THE BRAIN WITH VERY STRONG EXPRESSION IN THE
CC HIPPOCAMPUS, PIRIFORM CORTEX, AND THE SUPRACHIASMATIC NUCLEUS.
CC -1- INDUCTION: BY MITOGENS AND BY STRESS.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -1- SIMILARITY: Contains 1 rhodanese domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U23438; AAC52493.1; -
CC HSSP: Q16828; IMKP.
CC InterPro: IPR000340; DS_phosphatase.
CC InterPro: IPR001763; Rhodanese-like.
CC InterPro: IPR000387; TYR_phosphatase.
CC Pfam: PR00782; DSPC; 1.
CC SMART: PF00581; Rhodanese; 1.
CC SMART: SM00195; DSPC; 1.
CC SMART: SM00450; RHOD; 1.
CC PROSITE: PS50206; RHODANASE 3; 1.
CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
CC KEGG: K01195; Rhodanese; 1.
CC HYDROLASE; Nuclear protein.
CC FT DOMAIN 42 160 RHODANASE.
CC FT ACT SITE 188 395 PROTEIN-TYROSINE PHOSPHATASE.
CC FT ACT SITE 281 281 BY SIMILARITY.
CC SQ SEQUENCE 395 AA; 43187 MW; A90BFPD378A050FDF CR664;

Query Match 6.3%; Score 215.5; DB 1; Length 395;
Best Local Similarity 22.7%; Pred. No. 3.3e-06;
Matches 87; Conservative 54; Mismatches 130; Indels 113; Gaps 10;

QY 176 DDGGFSYVTSGGQSRIFKRSIQTMWATLQVLRQACBALSGIVPGSALTW----- 228
DB 22 DENGCTAGSSGSS-----HGAL-----GLISGKCLLDGRPLA 56
QY 229 --ASHYQERLNSQSCLENTA--NADLESJRPSPAEFGSSSEDEQMOAIRAEIMKYL 284
DB 57 HSAGYIRGSVNVRCNTIVRRRAKGSVSLQILP-----AEEVVARLRSGLYSAVI 107
QY 285 VSDLESVTSKEIRLELRGLPLQGYRDFID-NOMLLVAQRDRAS----- 330
DB 108 VYDERSPAESLRE--DSTVSLVQALRRNAERDIDCLKGYEFSSEYEPFCSKTKAL 165
QY 331 -----RIFPHLYGSEWNAANLEELQNRVTH 357
DB 166 AAIPEPVPSTVESLDGSSCGPTLHDGGVVELPLVLYGSAVHARMDALGITA 225
QY 358 ILNARELDNRYPEPFYTHNVRMLDESAQLPHMKETHRIEAPRAGQTHVLVCKMGV 417
DB 226 LLNVSSDCPNHFEHYQKCIPEVDNHRADISSWMEIAEYIDAVKCRGRVLVHCAGI 285
QY 418 SRSATVLAAMKQYCSLEQALRHVQELRIAPRNPGLTQ-IOYQGITASRQSHW 476
DB 286 SRSATICLAYLMKQRVLEAEFEVYKORRSIISBNSFMQQLLOFESQVLTLS----- 339
QY 477 EOKYGVSPDEHPAPEVSTPPPL 500
DB 340 -----CAAEASPSGFL 351
```

```
RESULT 15
VHP1 CAEEL STANDARD; PRT; 619 AA.
ID VHP1 CAEEL
AC Q10038;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase vhp-1 (EC 3.1.3.48).
GN VHP-1 OR F0881.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pseudocercariae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Chisoe S.;
RU Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U23178; AAC46719.1; -
CC PIR: T15969; T15969.
CC HSSP: Q16828; IMKP.
CC Wormpep: F0881.1; CE01899.
CC InterPro: IPR000340; DS_phosphatase.
CC InterPro: IPR000387; TYR_phosphatase.
CC Pfam: PR00782; DSPC; 1.
CC SMART: SM00195; DSPC; 1.
CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
CC KEGG: K01195; Rhodanese; 1.
CC HYDROLASE.
CC FT DOMAIN 200 269 PROTEIN-TYROSINE PHOSPHATASE.
CC FT DOMAIN 92 95 POLY-SER.
CC FT DOMAIN 351 354 POLY-SER.
CC FT DOMAIN 465 472 POLY-SER.
CC FT DOMAIN 483 488 POLY-SER.
CC FT ACT SITE 224 224 BY SIMILARITY.
CC SQ SEQUENCE 619 AA; 66354 MW; 369E326F615D0929 CR64;

Query Match 6.2%; Score 210.5; DB 1; Length 619;
Best Local Similarity 20.9%; Pred. No. 1.2e-05;
Matches 113; Conservative 66; Mismatches 198; Indels 163; Gaps 18;

QY 268 QEOMEQAIRAEIMKYL-----VSDLESVTSKEIRLELR-----GLPL----- 308
DB 40 RELEEDTDKRSRNVLEEDQPVSLPTPAKKGKGLQLTITSSPNTSSPSSSPTNG 99
QY 309 -----QGYRDFID-----NOMLLVAQRDRASRIFPHLYGSEWNAANLEEL 350
DB 100 GFRQFAQYFOLCESSEGMTRLPQSLQPTGDTLITLPNTYLSQIDSLDETWL 159
QY 351 QNRVTHILNMA-----REINDFPERFTYHNRMLDESAQLPHMKETHRIE 401
DB 160 DALDISVNTLSITCKSKVCIKEDKNFM-----RIPNDYQELSLSPFMAVEFEK 212
QY 402 ARAQGVTHVCKMGVRSAAVLAAMKQYCSLEQALRHVQELRIAPRNPGLTQ 461
DB 213 CRAGKCKLIHCLAGISRSPTLAISVIMRYMVGSDADAVRYKERRPSISPFNFVQQL 272
```

OY 462 IYQIL-----TASR-----QSHVMEQY-----GVSPPEHHA-- 490
Db 273 EYENVLIKDHVLDYNQASRPHRMDYYPDLCPKVPKASNCVFPSTHDESSPSP 332
OY 491 -----PEVST-----PFP-----LPPE 503
Db 333 SVSBSASAEPFTSSSAASSSTASAPSPSTSEQTSCTVNVNGKXMTMDLGLPHR 392
OY 504 PEGGGEKVVGMESQ-AAPKEP-----PGR-----PRNLRGVM 538
Db 393 PKALGLPSRIGTSVAELPSPSTELSRLSFNGPEALAPSTPIUNFTNCFNSPIIPVASS 452
OY 539 RSISLPEPSLESTSETSDMPEV-FSSHSSHEPL--OPPQLARTKGGQVDRGPQ 594
Db 453 REVILITPTPAASSSSTSESPSPSPSSSSSIYVENPPFASTVTPAGSSISTPS 512
OY 595 PALKRSQSVTLQGSVAVNFTQAFQEQEQGGGQGPICISTPRFRKVVQASVHDG 654
Db 513 --GQSTPASASSSAAARCMKGFVKKAPASTSTPASSTPGTSRAARPECLRSSG 569

Search completed: January 15, 2004, 06:49:52
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 15, 2004, 06:41:46 ; Search time 40 Seconds
(without alignments)
4251.417 Million cell updates/sec

Title: US-09-955-732-2

Perfect score: 3412
Sequence: 1 MALVTVSRSPGSGASTPVG.....RRKVVROAVHSDGEGEA 659

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------------|
| 1 | 3404 | 99.8 | 659 | 4 | Q8TE77 homo sapien |
| 2 | 2637 | 77.0 | 649 | 11 | Q8R330 mus musculu |
| 3 | 2633 | 76.9 | 513 | 4 | Q8N9L8 homo sapien |
| 4 | 2422 | 71.0 | 471 | 4 | Q8WY10 homo sapien |
| 5 | 1884.5 | 55.2 | 394 | 4 | Q9NWZ7 homo sapien |
| 6 | 1564 | 45.8 | 299 | 4 | Q9BQ20 homo sapien |
| 7 | 1172 | 34.3 | 692 | 4 | Q8WY14 homo sapien |
| 8 | 1172 | 34.3 | 1049 | 4 | Q8WY15 homo sapien |
| 9 | 1136 | 33.3 | 703 | 4 | Q8N9A7 homo sapien |
| 10 | 1133 | 33.2 | 464 | 11 | Q8C241 mus musculu |
| 11 | 1089.5 | 31.9 | 449 | 5 | Q8WY12 homo sapien |
| 12 | 940.5 | 27.6 | 1045 | 5 | Q9NXY1 Q9NXY1 diosophila |
| 13 | 918.5 | 26.9 | 1193 | 5 | Q8IMU8 Q8IMU8 diosophila |
| 14 | 581.5 | 17.0 | 141 | 4 | Q9NV45 homo sapien |
| 15 | 416.5 | 12.2 | 738 | 4 | Q9P2P8 homo sapien |
| 16 | 405 | 11.9 | 127 | 4 | Q8TDB5 Q8TDB5 homo sapien |

| | | | | | |
|----|-------|------|------|----|---------------------------|
| 17 | 366.5 | 10.7 | 195 | 4 | Q96H36 Q96H36 homo sapien |
| 18 | 358.5 | 10.5 | 195 | 4 | Q8WY11 Q8WY11 homo sapien |
| 19 | 322 | 9.4 | 202 | 4 | Q96F40 Q96F40 homo sapien |
| 20 | 310.5 | 9.1 | 148 | 4 | Q8WY13 Q8WY13 homo sapien |
| 21 | 288 | 8.4 | 198 | 10 | Q9ZK37 Q9ZK37 arabidopsi |
| 22 | 288 | 8.4 | 198 | 10 | Q9LUG6 Q9LUG6 mus musculu |
| 23 | 269.5 | 7.9 | 220 | 11 | Q9DEP6 Q9DEP6 mus musculu |
| 24 | 269.5 | 7.9 | 220 | 11 | Q8K4T5 Q8K4T5 mus musculu |
| 25 | 269.5 | 7.9 | 220 | 11 | Q92N12 Q92N12 mus musculu |
| 26 | 268 | 7.9 | 660 | 11 | Q920R2 Q920R2 mus musculu |
| 27 | 268 | 7.9 | 677 | 11 | Q99W66 Q99W66 mus musculu |
| 28 | 258 | 7.6 | 662 | 4 | Q81VY8 Q81VY8 homo sapien |
| 29 | 253.5 | 7.4 | 616 | 4 | Q8N5T1 Q8N5T1 homo sapien |
| 30 | 250.5 | 7.3 | 162 | 11 | Q9CRR3 Q9CRR3 mus musculu |
| 31 | 247.5 | 7.3 | 665 | 4 | Q96N49 Q96N49 homo sapien |
| 32 | 246.5 | 7.2 | 227 | 5 | Q95XK5 Q95XK5 caenorhadi |
| 33 | 246.5 | 7.1 | 196 | 10 | Q8LPG0 Q8LPG0 cryza sativ |
| 34 | 239 | 7.0 | 1042 | 4 | Q9C0D8 Q9C0D8 homo sapien |
| 35 | 233.5 | 6.8 | 483 | 11 | Q9CZY9 Q9CZY9 mus musculu |
| 36 | 233.5 | 6.8 | 483 | 11 | Q8R1L3 Q8R1L3 mus musculu |
| 37 | 233 | 6.8 | 622 | 11 | Q99MG5 Q99MG5 mus musculu |
| 38 | 233.5 | 6.8 | 167 | 10 | Q9M6K7 Q9M6K7 arabidopsi |
| 39 | 232.5 | 6.8 | 483 | 11 | Q9ESS0 Q9ESS0 mus musculu |
| 40 | 232.5 | 6.8 | 943 | 10 | Q8L4Z7 Q8L4Z7 cryza sativ |
| 41 | 232 | 6.8 | 184 | 11 | Q99N11 Q99N11 mus musculu |
| 42 | 229 | 6.7 | 295 | 4 | Q8N8Z6 Q8N8Z6 homo sapien |
| 43 | 228.5 | 6.7 | 184 | 4 | Q9NRW4 Q9NRW4 homo sapien |
| 44 | 227 | 6.7 | 177 | 11 | Q9C5L5 Q9C5L5 mus musculu |
| 45 | 227 | 6.7 | 1543 | 5 | Q9GV71 Q9GV71 dictyostell |

ALIGNMENTS

| | | | | |
|-----------------------|---|--------------|------|---------|
| RESULT 1 | Q8TE77 | PRELIMINARY; | PRT; | 659 AA. |
| ID | Q8TE77 | | | |
| AC | Q8TE77 | | | |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Created) | | | |
| DT | 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE | Hypothetical protein FLJ23852. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T., | | | |
| RA | Suzuki Y., Oiyashi M., Nishi T., Shibahara T., Tanaka T., | | | |
| RA | Nakamura Y., Isono T., Sugano S., | | | |
| RT | "NEDO human cDNA sequencing project"; | | | |
| RL | Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | HSSP; AK074432; BAB85080.1; -. | | | |
| DR | HSSP; Q16828; IMKP. | | | |
| DR | InterPro; IPR000340; DS_phosphatase. | | | |
| DR | InterPro; IPR000387; TYR_phosphatase. | | | |
| DR | Pfam; PF00782; DSPC; 1. | | | |
| DR | SMART; SM00195; DSPC; 1. | | | |
| DR | PROSITE; PS00066; TYR_PHOSPHATASE_2; 1. | | | |
| DR | PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1. | | | |
| KW | Hypothetical protein. | | | |
| SQ | SEQUENCE 659 AA; 72935 MW; 0D96E36F1FE81D3B CRC64; | | | |
| Query Match | 99.8%; Score 3404; DB 4; Length 659; | | | |
| Best Local Similarity | 99.8%; Pred. No. 5.7e-238; | | | |
| Matches | 658; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | |
| QY | 1 MALVTVSRSPGSGASTPVGFWDAVORRRLQRRGFAVLGAVLGGDNDAAEA 60 | | | |
| DB | 1 MALVTVSRSPGSGASTPVGFWDAVORRRLQRRGFAVLGAVLGGDNDAAEA 60 | | | |
| QY | 61 SSEPTEKAPSEELHGDPTDGGSGSPQKEBQRHLHMLVQLRQDDIRLAAGLEAP 120 | | | |

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Db 61 SSEPTKAPSEELHGDQTDFFGSGSPKQGEQOHLHMLVQLLRPODDITLAAQLAP 120
Qy 121 RPRRLAYLLVSTRBEGSLQDETVLLGVDFPDSSSPCTGLVPLMSDTQVYLDGGG 180
Db 121 RPRRLAYLLVSTRBEGSLQDETVLLGVDFPDSSSPCTGLVPLMSDTQVYLDGGG 180
Qy 181 FSVTSGGQRIFFKPSISIQTMMAITLQVHLQACEAALGSLVPGSALTWASHYQERLNSQ 240
Db 181 FSVTSGGQRIFFKPSISIQTMMAITLQVHLQACEAALGSLVPGSALTWASHYQERLNSQ 240
Qy 241 SCINEMTAMADESLRPPSAEPGSGSEQOMEOAIRAEIMKVLVDVSDLESVTSKEIRQA 300
Db 241 SCINEMTAMADESLRPPSAEPGSGSEQOMEOAIRAEIMKVLVDVSDLESVTSKEIRQA 300
Qy 301 ELRLGLPLOCYRDFINQMLLVAAQDRASRIFFPHYLIGSEWMAANLEELQKRVTHILN 360
Db 301 ELRLGLPLOCYRDFINQMLLVAAQDRASRIFFPHYLIGSEWMAANLEELQKRVTHILN 360
Qy 361 MAREIDNFFPERFTYNNVLMDEESQALLPHWKEITHRIEARAQCTHVLVHCKGVSR 420
Db 361 MAREIDNFFPERFTYNNVLMDEESQALLPHWKEITHRIEARAQCTHVLVHCKGVSR 420
Qy 421 AATVLAAYAMKQYECSEALRHVQELRPAPNPGLRQLOIYQGLITASRQSHWEQV 480
Db 421 AATVLAAYAMKQYECSEALRHVQELRPAPNPGLRQLOIYQGLITASRQSHWEQV 480
Qy 481 GGVSPPEHPAPEVSTFPPLPPEPEGGEKVVGMESQAAPKEBPFRINLGVKRS 540
Db 481 GGVSPPEHPAPEVSTFPPLPPEPEGGEKVVGMESQAAPKEBPFRINLGVKRS 540
Qy 541 ISLLEPSLESESTSESDMEPVFSSHSSHEEPLOFPOLARTKGQOQVDRPOPALSR 600
Db 541 ISLLEPSLESESTSESDMEPVFSSHSSHEEPLOFPOLARTKGQOQVDRPOPALSR 600
Qy 601 QSVVTLQGSAYVANRTOAFQEOEGQGGQGGECISSTPRFKVYRQASVHDSGEGEA 659
Db 601 QSVVTLQGSAYVANRTOAFQEOEGQGGQGGECISSTPRFKVYRQASVHDSGEGEA 659

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RESULT 2

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ID 08K330 PRELIMINARY; PRT; 649 AA.
AC 08K330;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to slingshot 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: B028922.1; A028922.1;
DR InterPro: IPR000340; DS phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSpC; 1.
DR SMART: SM00195; DSpC; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_DUAL; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 649 AA; 73227 MW; DF658B5E007E6F0 CRC64;

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Query Match 77.0%; Score 2627; DB 11; Length 649;
Best Local Similarity 80.3%; Pred. No. 1e-181;
Matches 530; Conservative 44; Mismatches 74; Indels 12; Gaps 7;

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Qy 1 MALVTASRSPGSGASTPVG-WDQVQRSRRLQRRQSFVLRGAVLGLQDGGDNDAAE 59
Db 1 MALVTASRSPGSGASTPVG-WDQVQRSRRLQRRQSFVLRGAVLGLQDGGDNDAAE 59

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Qy 60 ASSEPTKAPSEELHGDQTDFFGSGSPKQGEQOHLHMLVQLLRPODDITLAAQLA 119
Db 61 ADSEPMSEBPGECEPTEDQTDKQGLQSPWKQ-VQKRHLHMLWELLRPQDDITLAAQLA 119
Qy 120 RPRRLAYLLVSTRBEGSLQDETVLLGVDFPDSSSPCTGLVPLMSDTQVYLDGGG 179
Db 120 RPRRLAYLLVSTRBEGSLQDETVLLGVDFPDSSSPCTGLVPLMSDTQVYLDGGG 179
Qy 180 FSVTSGGQRIFFKPSISIQTMMAITLQVHLQACEAALGSLVPGSALTWASHYQERLNSQ 239
Db 180 FSVTSGGQRIFFKPSISIQTMMAITLQVHLQACEAALGSLVPGSALTWASHYQERLNSQ 239
Qy 240 QSCINEMTAMADESLRPPSAEPGSGSEQOMEOAIRAEIMKVLVDVSDLESVTSKEIRQA 299
Db 240 QSCINEMTAMADESLRPPSAEPGSGSEQOMEOAIRAEIMKVLVDVSDLESVTSKEIRQA 299
Qy 297 LEIRLGLPLOCYRDFINQMLLVAAQDRASRIFFPHYLIGSEWMAANLEELQKRVSHIL 356
Db 297 LEIRLGLPLOCYRDFINQMLLVAAQDRASRIFFPHYLIGSEWMAANLEELQKRVSHIL 356
Qy 360 MAREIDNFFPERFTYNNVLMDEESQALLPHWKEITHRIEARAQCTHVLVHCKGVSR 419
Db 360 MAREIDNFFPERFTYNNVLMDEESQALLPHWKEITHRIEARAQCTHVLVHCKGVSR 419
Qy 420 SAATVLAAYAMKQYECSEALRHVQELRPAPNPGLRQLOIYQGLITASRQSHWEQV 479
Db 420 SAATVLAAYAMKQYECSEALRHVQELRPAPNPGLRQLOIYQGLITASRQSHWEQV 479
Qy 479 GGVSPPEHPAPEVSTFPPLPPEPEGGEKVVGMESQAAPKEBPFRINLGVKRS 536
Db 479 GGVSPPEHPAPEVSTFPPLPPEPEGGEKVVGMESQAAPKEBPFRINLGVKRS 536
Qy 540 ISLLEPSLESESTSESDMEPVFSSHSSHEEPLOFPOLARTKGQOQVDRPOPALSR 599
Db 540 ISLLEPSLESESTSESDMEPVFSSHSSHEEPLOFPOLARTKGQOQVDRPOPALSR 599
Qy 599 QSVVTLQGSAYVANRTOAFQEOEGQGGQGGECISSTPRFKVYRQASVHDSGEGEA 659
Db 599 QSVVTLQGSAYVANRTOAFQEOEGQGGQGGECISSTPRFKVYRQASVHDSGEGEA 659

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RESULT 3

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ID 08N9L8 PRELIMINARY; PRT; 513 AA.
AC 08N9L8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein FLJ36907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Cerebellum;
RA Tangiani A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Oro T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kiyuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RA "NEBO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK034226; BAC04314.1;
DR InterPro: IPR000340; DS phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSpC; 1.
DR SMART: SM00195; DSpC; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.

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KM Hypothetical protein; Kinase.
SQ SEQUENCE 513 AA; 56909 MW; 7F1FDA03C229A09 CRC64;

Query Match 76.9%; Score 2623; DB 4; Length 513;
Best Local Similarity 99.0%; Pred. No. 1,4e-181;
Matches 506; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

151 FP--DSSSPCTGLVPLMSDPTQVYLDGSGFSYTSGGQSRIFKFISIQTMATIQVH 208
Db FPLSPASSPCTGLVPLMSDPTQVYLDGSGFSYTSGGQSRIFKFISIQTMATIQVH 62
QY QACEALGSGLVPGSALTWASHYQERLNSQCLNWTAMADLESIRPPSAEPGSSSQ 268
Db QACEALGSGLVPGSALTWASHYQERLNSQCLNWTAMADLESIRPPSAEPGSSSQ 122
QY EQMEQAIRALMVLVSDLESYTSKEIRQALRLRGLPQQYRDIQNDQMLLVQR 328
Db EQMEQAIRALMVLVSDLESYTSKEIRQALRLRGLPQQYRDIQNDQMLLVQR 182
QY ASFIPEHLVYSGSWMANLEELQNRVTHILNMAEIDNFPERTYHNVRIMDESSAQ 388
Db ASFIPEHLVYSGSWMANLEELQNRVTHILNMAEIDNFPERTYHNVRIMDESSAQ 242
QY LPWKETHRPIEARKQGHVLVHCKMGVSRSAATVLAAMQYECSLRQALRHVQELRP 448
Db LPWKETHRPIEARKQGHVLVHCKMGVSRSAATVLAAMQYECSLRQALRHVQELRP 302
QY IARPNGFLRQIQIYQIGILTASRQSHWEQYGVSPREEHPADEVSTPPPLPREEGG 508
Db IARPNGFLRQIQIYQIGILTASRQSHWEQYGVSPREEHPADEVSTPPPLPREEGG 362
QY EEKVGMESQAPKKEPPRPRIINRGWRSISLEPSELSESTDMEEVPSHRS 568
Db EEKVGMESQAPKKEPPRPRIINRGWRSISLEPSELSESTDMEEVPSHRS 422
QY SHEEPQPPQARLTGGQGVDRGPQALPKRSQSVTLGSAVVARQAPQEQSGQ 628
Db SHEEPQPPQARLTGGQGVDRGPQALPKRSQSVTLGSAVVARQAPQEQSGQ 482
QY 629 GQGPCISSTPRRKAVRQASVHDSGESEA 659
Db 483 GQGPCISSTPRRKAVRQASVHDSGESEA 513

RESULT 4
Q8WYLO PRELIMINARY; PRT; 471 AA.
ID Q8WYLO;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE HSSH-3.
GN HSSH-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21922082; PubMed-11832213;
RA Niwa R., Nagata-Ohashi K., Takeichi M., Mizuno K., Uemura T.,
RT "Control of Actin Reorganization by Slingshot, a Family of
Cell 108:233-246(2002).
DR EMBL; AB073360; BAB84119.3; -
DR HSSP; Q16828; IMR;
DR InterPro; IPR000340; DS_Phosphaase.
DR InterPro; IPR000387; TYR_Phosphaase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SMC0195; DSPC; 1.
DR PROSITE; PSS0086; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PSS0084; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 471 AA; 52741 MW; CE4E7F6F562B2D CRC64;

Query Match 71.0%; Score 2422; DB 4; Length 471;
Best Local Similarity 99.8%; Pred. No. 4,4e-161;
Matches 468; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MALVVSRRSPGSGASTPVGPMDQAVQRSLQRQSFALRGAVLGLQDGGDNDAAEA 60
Db 1 MALVVSRRSPGSGASTPVGPMDQAVQRSLQRQSFALRGAVLGLQDGGDNDAAEA 60
QY SSEPTKAPSEELHGDQTDFGQSGSPQKEEORQHLHWQLRPDDIRLAQLAP 120
Db SSEPTKAPSEELHGDQTDFGQSGSPQKEEORQHLHWQLRPDDIRLAQLAP 120
QY RPPRLRYLVSTRGEGLSODETVLGVDPDSSPSCCTGLVPLMSDPTQVYLDGSG 180
Db RPPRLRYLVSTRGEGLSODETVLGVDPDSSPSCCTGLVPLMSDPTQVYLDGSG 180
QY 121 RPPRLRYLVSTRGEGLSODETVLGVDPDSSPSCCTGLVPLMSDPTQVYLDGSG 180
Db 121 RPPRLRYLVSTRGEGLSODETVLGVDPDSSPSCCTGLVPLMSDPTQVYLDGSG 180
QY 181 FSVTSGGSGRIFKFISIQTMATIQVHQAEEALGSGLVPGSALTWASHYQERLNSQ 240
Db 181 FSVTSGGSGRIFKFISIQTMATIQVHQAEEALGSGLVPGSALTWASHYQERLNSQ 240
QY 241 SCLEWMTAMADLESIRPPSAEPGSSSQEQMEQAIRALMVLVSDLESYTSKEIRQAL 300
Db 241 SCLEWMTAMADLESIRPPSAEPGSSSQEQMEQAIRALMVLVSDLESYTSKEIRQAL 300
QY 301 ELRLGLPQQYRDIQNDQMLLVQRDRASRIFPHLYSGSWMANLEELQNRVTHILN 360
Db 301 ELRLGLPQQYRDIQNDQMLLVQRDRASRIFPHLYSGSWMANLEELQNRVTHILN 360
QY 361 MAREIDNFPERTYHNVRIMDESSAQILPWKETHRPIEARKQGHVLVHCKMGVSR 420
Db 361 MAREIDNFPERTYHNVRIMDESSAQILPWKETHRPIEARKQGHVLVHCKMGVSR 420
QY 421 AATVLAAMQYECSLRQALRHVQELRPIARPNGFLRQIQIYQIGILTA 469
Db 421 AATVLAAMQYECSLRQALRHVQELRPIARPNGFLRQIQIYQIGILTA 469

RESULT 5

Q9NMZ7 PRELIMINARY; PRT; 394 AA.
ID Q9NMZ7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein FLJ20515.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isegauchi S., Sugano S.,
RT "NEDO human cDNA sequencing project".
DR EMBL; AK000522; BAA91228.1; -
DR Hypothetical protein.
SQ SEQUENCE 394 AA; 42724 MW; F87C7F5A29048AAE CRC64;

Query Match 55.2%; Score 1884.5; DB 4; Length 394;
Best Local Similarity 59.8%; Pred. No. 2,9e-128;
Matches 394; Conservative 0; Mismatches 0; Indels 265; Gaps 1;

1 MALVVSRRSPGSGASTPVGPMDQAVQRSLQRQSFALRGAVLGLQDGGDNDAAEA 60
Db 1 MALVVSRRSPGSGASTPVGPMDQAVQRSLQRQSFALRGAVLGLQDGGDNDAAEA 60
QY SSEPTKAPSEELHGDQTDFGQSGSPQKEEORQHLHWQLRPDDIRLAQLAP 120
Db 61 SSEPTKAPSEELHGDQTDFGQSGSPQKEEORQHLHWQLRPDDIRLAQLAP 120

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QY 121 REPRLRYLLVSTREGESLQDETVLLGVDPDSSPSCITGLVPLVMSDTQVYLDGPG 180
DB 121 REPRLRYLLVSTREGESLQDETVLLGVDPDSSPSCITGLVPLVMSDTQVYLDGPG 180
QY 181 FSVTSGGOSRIKPIKPISTQTMATLQVLAQACAAAGSLVPGSALTMASHYOERLNEQ 240
DB 181 FSVTSGGOSRIKPIKPISTQTMATLQVLAQACAAAGSLVPGSALTMASHYOERLNEQ 240
QY 241 SCINEMTAMADESLRPPSAEPGSGSECEOMQAIKRAELWKYLDVSDLESVTSKEIRQAL 300
DB 241 SCINEMTAMADESLRPPSAEPGSGSECEOMQAIKRAELWKYLDVSDLESVTSKEIRQAL 300
QY 301 EIRLGLPLQOYDFIDNOMLLVLAQRDRASRLFPHLVYLGSEMANANLELOQRNRYTHLN 360
DB 283 ----- 282
QY 361 MAREIDNFERFTYHNANVLMDESAQLPFWKETHRFTEAARAOQTHLVHCKMVSRS 420
DB 283 ----- 282
QY 421 AATVLAANKOYECGLEQALRHVQELRPIARPNGFLRQLOLYQGLTASRQSHVEQKV 480
DB 283 ----- 282
QY 481 GGVSPPEHPAPEVSTFPPLPPEPEGGGEKVVGMESQAAPKEBGPRLNLRGMRS 540
DB 283 ----- 282
QY 541 ISLLEPSLEESTSETSDMPEVSSHESHEEPLQFPOLARTKGQOYDRGPALKSR 600
DB 283 ----- 282
QY 601 QSVYTLQGSANVANRTOAFQEQGQGGQGGEPICISSTRFRKVVYQASVHDSGEDEA 659
DB 336 QSVYTLQGSANVANRTOAFQEQGQGGQGGEPICISSTRFRKVVYQASVHDSGEDEA 394

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RESULT 6

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Q98Q20 PRELIMINARY; PRT; 299 AA.
ID Q98Q20
AC Q98Q20;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Similar to hypothetical protein FLJ10928.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004210; AA04210.1;
DR EMBL; BC004176; AA04176.1;
DR HSSP; P51452; IYR.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 299 AA; 33289 MW; 30C4BFEC16A23380 CRC64;

```

Query Match 45.8%; Score 1564; DB 4; Length 299;
 Best Local Similarity 100.0%; Pred. No. 3.1e-105;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 361 MAREIDNFERFTYHNANVLMDESAQLPFWKETHRFTEAARAOQTHLVHCKMVSRS 420
DB 1 MAREIDNFERFTYHNANVLMDESAQLPFWKETHRFTEAARAOQTHLVHCKMVSRS 60
QY 421 AATVLAANKOYECGLEQALRHVQELRPIARPNGFLRQLOLYQGLTASRQSHVEQKV 480

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DB 61 AATVLAANKOYECGLEQALRHVQELRPIARPNGFLRQLOLYQGLTASRQSHVEQKV 120
QY 481 GGVSPPEHPAPEVSTFPPLPPEPEGGGEKVVGMESQAAPKEBGPRLNLRGMRS 540
DB 121 GGVSPPEHPAPEVSTFPPLPPEPEGGGEKVVGMESQAAPKEBGPRLNLRGMRS 180
QY 541 ISLLEPSLEESTSETSDMPEVSSHESHEEPLQFPOLARTKGQOYDRGPALKSR 600
DB 181 ISLLEPSLEESTSETSDMPEVSSHESHEEPLQFPOLARTKGQOYDRGPALKSR 240
QY 601 QSVYTLQGSANVANRTOAFQEQGQGGQGGEPICISSTRFRKVVYQASVHDSGEDEA 659
DB 241 QSVYTLQGSANVANRTOAFQEQGQGGQGGEPICISSTRFRKVVYQASVHDSGEDEA 299

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RESULT 7

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Q9WYL4 PRELIMINARY; PRT; 692 AA.
ID Q9WYL4
AC Q9WYL4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE HSSH-1S.
GN HSSH-1S.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21822082; Pubmed=11832213;
RA Niva R., Nagata-Ohashi K., Takeichi M., Mizuno K., Uemura T.;
RT "Control of Actin Reorganization by Slingshot, a Family of
RT Phosphatases that Dephosphorylate Adf/Cofilin."
RL Cell 108:233-246 (2002).
DR EMBL; AB072356; BAB84115.1;
DR HSSP; Q16828; IYKP.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 692 AA; 77430 MW; 9DC1FF2C8984384 CRC64;

```

Query Match 34.3%; Score 1172; DB 4; Length 692;
 Best Local Similarity 42.3%; Pred. No. 2.4e-76;
 Matches 269; Conservative 95; Mismatches 170; Indels 102; Gaps 18;

```

QY 1 MALTVASRPPGSGASTPVGWMD-----QAVQSRRLQROSPFVLRGAVLGLDDGDNDD 56
DB 1 MALTVASRPPGSGASTPVGWMD-----QAVQSRRLQROSPFVLRGAVLGLDDGDNDD 56
QY 57 AABASSEPTKAPSEELHGDQTFQGS-QSPQKCE-EORHILHMLWQILRPDDIRLA 114
DB 57 AABASSEPTKAPSEELHGDQTFQGS-QSPQKCE-EORHILHMLWQILRPDDIRLA 114
QY 56 -----SSPQ-----GQRSLQHPKXAGDLPQHLQVWIMNLRCEDRKILA 94
DB 56 -----SSPQ-----GQRSLQHPKXAGDLPQHLQVWIMNLRCEDRKILA 94
QY 115 AQLAPRPPRIYLLV--STRSGEGLSODETVLLGVDPDSSPSCITGLVPLVMSDTQ 172
DB 115 AQLAPRPPRIYLLV--STRSGEGLSODETVLLGVDPDSSPSCITGLVPLVMSDTQ 172
QY 95 VRLSEAMADRVRYVVVVVSSGRC---DTEENILLYGVDFSSKSKSCITIMVRLWSDTK 150
DB 95 VRLSEAMADRVRYVVVVVSSGRC---DTEENILLYGVDFSSKSKSCITIMVRLWSDTK 150
QY 173 VYLDGGGFGFVTSGGGRIKPIKPISTQTMATLQVLAQACAAAGSLVPGSALTMASHY 232
DB 173 VYLDGGGFGFVTSGGGRIKPIKPISTQTMATLQVLAQACAAAGSLVPGSALTMASHY 232
QY 151 IHLGGDGFVSTGRMHITFPVSVQMMKALQVLAQACAAAGSLVPGSALTMASHY 210
DB 151 IHLGGDGFVSTGRMHITFPVSVQMMKALQVLAQACAAAGSLVPGSALTMASHY 210
QY 223 QERINSEQSCINEMTAMADESLR--PSAEPGSGSECEOMQAIKRAELWKYLDVSDLE 290
DB 223 QERINSEQSCINEMTAMADESLR--PSAEPGSGSECEOMQAIKRAELWKYLDVSDLE 290
QY 211 ESCISSEQSCINEMTAMADESLRPSALFVDFKTEGERTERLIKAKLSIMMSODLEN 270
DB 211 ESCISSEQSCINEMTAMADESLRPSALFVDFKTEGERTERLIKAKLSIMMSODLEN 270
QY 291 VTSKEIRNELEKQNMCKELKEFTIDNEMLLILQMDKPSLIFPHLVLGSEMANANLEEL 350
DB 291 VTSKEIRNELEKQNMCKELKEFTIDNEMLLILQMDKPSLIFPHLVLGSEMANANLEEL 350
QY 271 VTSKEIRNELEKQNMCKELKEFTIDNEMLLILQMDKPSLIFPHLVLGSEMANANLEEL 330

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QY 351 ORNRVTHLNMAREIDNFEYPERFYHNVRLMDEESAQLPHMKETHRFIEAARQGHVL 410
DB 331 QSGGVYIILNVTREINFEFGLEFAYNINRYDEETDILAHMWEAHPINAKRHNKSKL 390
QY 411 VHCXGVSSAATVLAAYAMKQYECLEQALRHVQELPIARPNGFLRQLOIYQIGILTAS 470
DB 391 VHCXGVSSASATVLAAYAMKEFGWPLEKAYNVKQKSIIRPNAGFMROLSEYEGILDAS 450
QY 471 RQSH--VWEQVGG--VSPENHPA-----PEVSTPF-----PRLP-- 501
DB 451 KQHNKLMRQQTDSILQOPVDDPAGPDLPETPDGTPESQLPFLDDAQPGLGPPLPCC 510
QY 502 -----PEPEGGEKVVGMEE-----SQAPKEE---PGPRPRINLGVMRS 540
DB 511 FRLSDPLPSPDEDTG---SLVHLEDPERALEEAPPAVHPRARQO-----QG 560
QY 541 ISLLEPSL--ELESTSETSDMEPEVFSHSHSHEPL 574
DB 561 SGLCEKDVKKKLEFGSPKGRSGSLQVETTEREGL 596

RESULT 8
Q8WY15 PRELIMINARY; PRT; 1049 AA.
AC Q8WY15;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE HSSH-1L.
GN HSSH-1L.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:21822082; PubMed:11832213;
RA Niva R.; Nagata-Ohnishi K.; Takeichi M.; Mizuno K.; Uemura T.;
RT "Control of Actin Reorganization by Slingshot, a Family of
RT Phosphatases that Dephosphorylate ADP/Cofilin."
RL Cell 108:233-246(2002).
DR EMBL; AB073355; BAB84114.1; -
DR HSSP; O16828; 1MKP.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 1049 AA; 115534 MW; 060C0FC75E17889C CRC64;

Query Match 34.3%; Score 1172; DB 4; Length 1049;
Best Local Similarity 42.3%; Pred. No. 44e-76;
Matches 269; Conservative 95; Mismatches 170; Indels 102; Gaps 18;

QY 1 MALVTVSRSPPGSGASTPVGPMW---QAVQRSHSLQKROSGPAVLGALGQGGNDMD 56
DB 1 MALVTILQNSPTSAASSASNSSELEAGSEEDRKLTLSSESEFVWKGALFLQGG---- 55
QY 57 AAEASSEPTKAPSEELHGDQTFGQGS-QSPQKE-EQOQHILMVLQQLRPDDIRLA 114
DB 56 -----SSPQ-----GQSLQHPHGHAGDLPQHQLQVWNLNLCRCEIRILA 94
QY 115 AQLAEPAPPRRLRYLLV--STRREGSLQODEFVLIGVFPSSSPSCSLGLVFLVMSTQ 172
DB 95 VLLSAMAADRYKRYVVVSSGRQ---DTEENILGVDFSSKESKSCITIGVLLMSTDK 150
QY 173 VYLDGDFGSVYSGQSSRIFKFISIQTMATLOVLHQAALGSGVPGGSALTWASHY 232
DB 151 IHLDDGDFGSVSTAKRMHIFKRVSVQAMWSALQVLHKKCEVARRHNHYPGVALIMATY 210
QY 233 QERLNSQSCINMTAMADLSLR--PSAEPGSSSEQEQMQLRAELMKVLDVSDLES 290

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DB 211 ESCISSESCINENNAQDLESTPDPSPALFVDKPTGERFRERILAKTASIMMSQLEN 270
QY 251 VTSXEIRQALRLGLPLQGYRDFIDNQMLLVAQRASRIFPHLYGSEWNAANTEEL 350
DB 271 VTSXEIRLELEKQKNCMLKEIKERIDNEMLLILQMKKPSLIFDHLVYGSEWNASNLEEL 330
QY 351 ORNRVTHLNMAREIDNFEYPERFYHNVRLMDEESAQLPHMKETHRFIEAARQGHVL 410
DB 331 QSGGVYIILNVTREINFEFGLEFAYNINRYDEETDILAHMWEAHPINAKRHNKSKL 390
QY 411 VHCXGVSSAATVLAAYAMKQYECLEQALRHVQELPIARPNGFLRQLOIYQIGILTAS 470
DB 391 VHCXGVSSASATVLAAYAMKEFGWPLEKAYNVKQKSIIRPNAGFMROLSEYEGILDAS 450
QY 471 RQSH--VWEQVGG--VSPENHPA-----PEVSTPF-----PRLP-- 501
DB 451 KQHNKLMRQQTDSILQOPVDDPAGPDLPETPDGTPESQLPFLDDAQPGLGPPLPCC 510
QY 502 -----PEPEGGEKVVGMEE-----SQAPKEE---PGPRPRINLGVMRS 540
DB 511 FRLSDPLPSPDEDTG---SLVHLEDPERALEEAPPAVHPRARQO-----QG 560
QY 541 ISLLEPSL--ELESTSETSDMEPEVFSHSHSHEPL 574
DB 561 SGLCEKDVKKKLEFGSPKGRSGSLQVETTEREGL 596

RESULT 9
Q8N9A7 PRELIMINARY; PRT; 703 AA.
AC Q8N9A7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Hypothetical protein FLJ38102.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nishimura K.; Nagatsuma M.; Kanda K.; Kondo H.; Yokoi T.; Kodaira H.;
RA Futuya T.; Takahashi M.; Kikkawa E.; Omura Y.; Abe K.; Kamihara K.;
RA Katsuta N.; Sato K.; Tanikawa M.; Yamazaki M.; Sugiyama T.; Irie R.;
RA Otsuki T.; Sato H.; Wakamatsu A.; Ishii S.; Yamamoto J.; Isono Y.;
RA Kawai-Hio Y.; Saito K.; Nakamura Y.; Sekine M.; Kikuchi K.; Yamashita H.;
RA Matsuo K.; Nakamura Y.; Oshima A.; Sugiyama A.; Kawakami B.;
RA Kanehori K.; Takahashi-Fujii A.; Masuno Y.; Negai K.; Isogai T.;
RA Suzuki Y.; Sugano S.; Nagahara K.; Masuno Y.; Negai K.; Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK095421; BA004546.1; -
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
KW Hypothetical protein.
SQ SEQUENCE 703 AA; 78978 MW; 3ACFABA4B97CBE7A CRC64;

Query Match 33.3%; Score 1136; DB 4; Length 703;
Best Local Similarity 42.9%; Pred. No. 1e-73;
Matches 256; Conservative 91; Mismatches 152; Indels 98; Gaps 17;

QY 36 QSFPAVLGAVLGLQDGDNDAAEASSEPTKAPSEELHGDQTFGQGS-QSPQKE-E 93
DB 51 ESFPFWKGAALFLQGG-----SSPQ-----GQSLQHPHGHAGD 84
QY 94 QRHILMVLQQLRPDDIRLAQLAEPAPPRRLRYLLV--STRREGSLQODEFVLIGVFP 151
DB 85 LPHQLQVWNLNLCRCEIRILAVALLESAMADRYKRYVVVSSGRQ---DTEENILGVDF 140

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QY 152 FDSSPSCCTGLVLTPLMSDPOVLTLDGSGFSVTSGGOSRIFKPISTQTMATLOVLAHOAC 211
 DB 141 SSKESKSCCTIGVLTPLMSDPTKIHLDGSGFSVTSAGMMHIFKVSQVQAMMSALQVLAHXC 200
 QY 212 EALGSGLVPGGSALTWASHYQERLNSQSCINEMWTAMADLESRLP--PSAEPGSSSECE 269
 DB 201 EVARHNHFFPGVALIMATWYESSCSISQSCINEMWMOQLESTRPDSPALFVDPKTEGE 260
 QY 270 QMEQARLAEKLVKVDVSDLESVTSKELRQALTELRGLPQGVDFPDNOMLLVVAORBA 329
 DB 261 RTEIRIKKASIMSDLEWVTSKELRNELEKQMNCKELKEFDENEMLLLGMDP 320
 QY 330 SRIFPHLYLGSEWNAANLEELQNRVTHILNMAEIDNFPERTYHNVRLWDESAQL 389
 DB 321 SLIFDHYLGSEWNAANLEELQSGVDYILNVTREIDNFPGLFAYHNIRVDEETDIL 380
 QY 390 PHWKETRFEIAAAGQTHVLVHCKMGVSRSAATVLAAMKQVCEGLBQALHVOELRI 449
 DB 381 AHMNEAYHFIKAKRNSKCLVHCKMGVSRSAATVLAAMKQVCEGLBQALHVOELRI 440
 QY 450 ARENPGFLQLOIYQILTAASQSH--VWEQVKG--VSEBHPA-----PE 492
 DB 441 TRPNAGFWBQLSEYEGILDASKQHNKLMQCTDSIQCPVDDPAGPDLFETPDTPE 500
 QY 493 VSTPF-----PPLP-----PEPGGGEKVGWME-----SOAP 522
 DB 501 SOLFLDDAOPGCGPLPCCFRRLSDPLPSPEDTG--SLVHLEDEREALLEBAP 557
 QY 523 KEE--PQPRRINLRGWRMSISLEPSL--ELESTSESDMEVESHSSHEBPL 574
 DB 558 PAEYHAPARQO-----QSGGLCEKDVKKLEFSPKORSGLILQVETEREEL 607

RESULT 10

Q8C241 PRELIMINARY; PRT; 464 AA.
 AC Q8C241;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to HSSH-1L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK089308; BAC40835.1;
 DR EMBL; AK089308; BAC40835.1;
 SQ SEQUENCE 464 AA; 52781 MW; 96B736009573DDBC CRC64;

Query Match 33.2%; Score 1133; DB 11; Length 464;
 Best Local Similarity 48.1%; Pred. No. 9.3e-74;
 Matches 232; Conservative 85; Mismatches 129; Indels 36; Gaps 7;

QY 1 MALVTYRSPPGSGASTPVGPMDAV-----QRRSRQROSFAVLGAVLGLQDGDND 56
 DB 1 MALVTYRSPPGSGASTPVGPMDAV-----QRRSRQROSFAVLGAVLGLQDGDND 56
 QY 57 AAEASSEPTKASEEELHGDQDFPGQS-QSPQKQE-EQRQHLHMLVQLRPQDITLA 114
 DB 56 -----NSPQ-----GQSLQHPKKAAGDLPHQLVWMLNLCERIKYLA 94
 QY 115 AQLEAPRPRLRYLLVSTREGELQSDETVLGVDFPDSSPSCCTIGVLTPLMSDPOV 174
 DB 95 VRLSEWVTRVRRVMVVVTSGRQ--DTEENILGLVDFSSKESKSCCTIGVLTPLMSDPTKH 152

QY 175 LDGSGFSVTSGGOSRIFKPISTQTMATLOVLAHOAC 234
 DB 153 LDGSGFSVTSAGMMHIFKVSQVQAMMSALQVLAHXC 212
 QY 235 RLSNQSCLNEMWTAMADLESRLP--PSAEPGSSSECEQMEQARLAEKLVKVDVSDLESVT 292
 DB 213 CISQSCINEMWMOQLESTRPDSPALFVDPKTEGERTERELIKKASIMSDLEWVTS 272
 QY 293 SKELRQALTELRGLPQGVDFPDNOMLLVVAORBASRIFPHLYLGSEWNAANLEELQ 352
 DB 273 SKELRQALTELRGLPQGVDFPDNOMLLVVAORBASRIFPHLYLGSEWNAANLEELQ 332
 QY 353 NRYTHILNMAEIDNFPERTYHNVRLWDESAQLPHWKETRFEIAAAGQTHVLVH 412
 DB 333 SGVDYILNVTREIDNFPGLFAYHNIRVDEETDILAHMNEAYHFIKAKRNSKCLVH 392
 QY 413 CKMGVSRSAATVLAAMKQVCEGLBQALHVOELPIARPNGFLQLOIYQILTAASQ 472
 DB 393 CKMGVSRSAATVLAAMKQVCEGLBQALHVOELPIARPNGFLQLOIYQILTAASQ 452
 QY 473 SH 474
 DB 453 RH 454

RESULT 11

Q8WY12 PRELIMINARY; PRT; 449 AA.
 AC Q8WY12;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE HSSH-2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21822082; PubMed=11832213;
 RA Niva R., Nagata-Onashi K., Takeichi M., Mizuno K., Uemura T.;
 RT "Control of Actin Reorganization by Slingshot, a Family of
 RT Phosphatases that Dephosphorylate ADF/Cofilin."
 RL Cell 108:233-246 (2002).
 DR EMBL; AB072358; BAB84117.1;
 DR HSSP; O16828; IMRP.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSEP; 1.
 DR SMART; SM00195; DSEP; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 SQ SEQUENCE 449 AA; 51492 MW; AFD156098492A04D CRC64;

Query Match 31.9%; Score 1089.5; DB 4; Length 449;
 Best Local Similarity 44.7%; Pred. No. 1.3e-70;
 Matches 215; Conservative 97; Mismatches 124; Indels 45; Gaps 5;

QY 1 MALVTYRSPPGSGASTPVGPMDAVQRRSRQRR--QSFARVLRGAVLGLQDGDND 57
 DB 1 MALVTYRSPPGSGASTPVGPMDAVQRRSRQRR--QSFARVLRGAVLGLQDGDND 53
 QY 58 AAEASSEPTKASEEELHGDQDFPGQS-QSPQKQE-----RQHLHMLVQLRPQD 110
 DB 54 -----GSSSTRIRSHRKVKKAAGDLQCHLQAMFILLREEDN 89
 QY 111 IRLAAGLEAPRPRLRYLLVSTREGELQSDETVLGVDFPDSSPSCCTIGVLTPLMSD 170
 DB 90 IRLAVALSESTYQNRIRRVVVSTNGRQ--DTEESIVLGMDPSSNDSTCTIGVLTPLMSD 147
 QY 171 TQVYLDGSGFSVTSGGOSRIFKPISTQTMATLOVLAHOAC 230

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DB 148 TLHLDGDFSVSTNRHIFKPVSVQAMMSALQSLHACVAAAHNYPSLSLTWS 207
QY 231 HYQERLNSQSCINEXTAMADLESIRP--PSAEPGGSSQEOQEOAIRAELMKVLDSVL 288
DB 208 YVESHINSQSSVNMAMQDVQSHRDPSPALFTDIPTERRETEKLITKLEIMMOQDL 267
QY 289 EYSTSKIRQALELRGLPQOVRPFDINOMLLVAQRBARIRPHLYLGSSEMAANLE 348
DB 268 ENTSKEITELBMQVNCVLRKEFDINEMTVLGGQDSPTQIEHVFHLSSEMAANLE 327
QY 349 ELQNRVTHILNMAREIDNPFERYTHANVRLMDESAQLPFWKETHRFIENARAQGT 408
DB 328 DLQNRGVRIILNVRIDNPFPGVEFYHNIIRYDEADTDLALVMDTYKFSKAKGSK 387
QY 409 VLVHCKMGVSRSAATVLAAMKQYEGSLQALRHVOELPPIARPNGPFRQIQYQIL 468
DB 388 CLVHCKMGVSRSAATVLAAMKQYEGSLQALRHVOELPPIARPNGPFRQIQYQIL 447
QY 469 A 469
DB 448 A 448

RESULT 12
Q9NXY1 PRELIMINARY: PRT: 1045 AA.
ID Q9NXY1 OSWY04:
AC 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 22, Last annotation update)
DE MAP kinase phosphatase (MAP-kinase-phosphatase protein).
SSH OR CG6238.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
OC Ephydroidea, Drosophilidae, Drosophila.
OC NCBI_Taxid=7227;
OX [1]
RN SEQUENCE FROM N.A.
RA Niwa R., Takeichi M., Temura T.,
RT "a novel MAP kinase phosphatase (Drosophila).",
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKee G.L.G.,
RA Abril J.F., Acharyani A., An H.-J., Andrews-Piankocch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glaser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Ibegun C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkllov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,

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RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,
RA Sine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svrtkars R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RL Science 287:2185-2195 (2000).
DR EMBL: AB036834; BAA89534.1;
DR EMBL: AB003750; AAF56372.2;
DR HSSP: Q16828; IMKP.
DR FlyBase: FBgn0029157; gsh.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR SMART: SM00195; DSPC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Kinase.
SQ SEQUENCE 1045 AA; 114996 MW; 76620BB63EE59A8B CRC64;

Query Match 27.6%; Score 940.5; DB 5; Length 1045;
Best Local Similarity 34.6%; Pred. No. 2,5e-59;
Matches 230; Conservative 96; Mismatches 219; Indels 119; Gaps 11;

QY 1 MALVTASRSPGSGA-STPVGPDQAVQVRSLQRQSFALRGAVLGLDGGNDDAE 59
DB 1 MALVTQSRSPVASCSNDSQSESDGKNDRSCEFGAGKTALVL----- 49
QY 60 ASSPTEKASEEELHDDQDFQGGSGSPQKQEQRHILHMQLARPODDIRLAQLEA 119
DB 50 ALKQIPULTQSERLSTDSSTRSNSTGS--NSDIOQLHLSMFYLLQREDTLKMAVLES 107
QY 120 PRPRRLRYLLVVS----- 132
DB 108 QRSNRTYLVLAASGCCRSQSDRRHRIMRHSHVYKVSAGTKSSSTSPAVPTQRLQSLVE 167
QY 133 -----TREGGLS---QDEFVLLGVDPDSSSSPSCGLVLPMSD 170
DB 168 QTATEASSCKDKTAKENATAGDNKNTSGMEBSCLIGDNCERT---TIGVVPILAD 223
QY 171 TQVVLDDGGFVSVTSGGSHIFKPISTIQTMATQVLAHQCEALAGSLVPGGSLTAS 230
DB 224 TTHLDGDFSVSVYVYKTHIFKPVSVQAMMSALQTLHKYSKAKENNFASGSHWLS 283
QY 231 HYQERLNSQSCINEXTAMADLESIRP--PSAEPGGSSQEOQEOAIRAELMKVLDSVL 288
DB 284 SYERISDSQSCINEMAMALSRPSPDAIRNKPKEKESVTKMKLKAIMSVLDL 343
QY 289 EYSTSKIRQALELRGLPQOVRPFDINOMLLVAQRBARIRPHLYLGSSEMAANLE 348
DB 344 DEVTSKIRGLEILDMVDEGKYSFTDAEMLVLLGMDAPTKIFEVHVLGSSEMAANLE 403
QY 349 ELQNRVTHILNMAREIDNPFERYTHANVRLMDESAQLPFWKETHRFIENARAQGT 408
DB 404 ELQNGVRHILNVRIDNPFPGVEFYHNIIRYDEADTDLALVMDTYKFSKAKGSK 463
QY 409 VLVHCKMGVSRSAATVLAAMKQYEGSLQALRHVOELPPIARPNGPFRQIQYQIL 468
DB 464 VLVHCKMGVSRSAATVLAAMKQYEGSLQALRHVOELPPIARPNGPFRQIQYQIL 523
QY 469 ASR-----QSHWEGKGVSPSEHPAPEV-----STPFPPLPEPEGGE 509
DB 524 AMKQKELQSKSKSTNLSKTKDARILPGSEPTPLIQALNQAQSKSLGEAVTDD--GEE 560
QY 510 EKVYGMESQAPKEEDPPRINLRGWSISLLEPSLLESTSETSDMPEVFSHSS 569
DB 581 EDGSRMRRSIAGSQ-----RRMVRSSSTSPKTCGAVVTKQSGSEMENLTPRSV 632

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QY 570 HEEP 573
DB 633 AEEP 636

RESULT 13
ID 081M08 PRELIMINARY; PRT; 1193 AA.
AC 081M08;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG6238-PB.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agayant A., An H.U., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.K.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Borchan D.A., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burks J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A.L., Deng Z., Mays R.D., Dew I., Dietz S.M.,
RA Dodson R., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glick A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kallal M., Kalish F., Kapen G.H., Ke Z., Kienin J.A., Kelchum K.A.,
RA Kimmel B.E., Koditz C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris C., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo K., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Strickas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodruff W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RA Celinkner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson R., Dorett V., Dou P.L.E., Doyle C., Drenek D., Farfan D.,
RA Fiertera K., Frise E., Galie R.F., Garg N.S., George R.A.,
RA Gonzalez W., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jatali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K., Nunoo J.,
RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Prounanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminck J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinkner S.E.,
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Seale S.M.D., Smith E., Shu S., Stutnak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Vungali C.J., Lewis S.E.,
RT "Annotation of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celinkner S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF003750; AAM14027.1; AIB9398A043FF1B CRC64;
SQ SEQUENCE 1193 AA; 131521 MW; AIB9398A043FF1B CRC64;
Query Match 26.9%; Score 918.5; DB 5; Length 1193;
Best Local Similarity 34.2%; Pred. No. 1.2e-57;
Matches 216; Conservative 96; Mismatches 192; Indels 131; Gaps 11;
49 QDGGDNDAAEASSEPERKA-----PSEELHNDQDFQGGSG 86
DB 20 RDGSEED-EGNSKNGDRSECFAGKGTALVIALDIPLOTSEERLSTDSRNSSTQ 77
QY SPQKEOROHLMVOLLPPODIRLAOLLEAPPRRLYLWVS-----132
DB 87 RDGSEED-EGNSKNGDRSECFAGKGTALVIALDIPLOTSEERLSTDSRNSSTQ 77
DB 78 S--NNSIQHLQSMFLLREDTLKAVVLESGRSRTYLVYARSCCRSGTSRRH 135
QY 133 -----TREGELS 140
DB 136 RIMRHSVKVGSAGTSTSPAVPTQRLSVQTLATASCKDKTADKENATPAAGGNK 195
QY 141 ---QDEVLLGVDPDPSSPSCTGLVPLMSPSTOVYLDGDFSVTSGQSRIFKPIST 197
DB 196 TSGMBESSCLGIDNERT---TIGLVPLIATTTIHDGDFSVYVYKTHFKVSV 251
QY 198 QTMATQVILHQAEEALGGLVPGSGALTWASHYGERLNEEGSCINEMTAMADLESLR 257
DB 252 QAMWALQTLHKVSKKARENMFYASGPHDMLSSYERIRIESDOSCLNEMWMDALBSRRP 311
QY 258 PSAP--GGSSEQOMQAIKRAELMKVLDVDSLESTSKRIQALELRGLPQOYRDFI 315
DB 312 PSPAIRNKPPEKETSIVKMKTKATWMSVDDEVTSKIRGLLEITLMDLGEYKFSI 371
QY 316 DNQMLLVAORDRASRIFPHVLGSEEMNANLEICNRYTHILNMAEIDNFPYPERFTY 375
DB 372 DAEMVLVIGMDATKTFEHVYLGSEEMNANLEICNRYTHILNMAEIDNFPYPERFTY 431
QY 376 HNVRLWDEESAQLIPHKETHRFLEAPARAGCTHYLVHCKGVGSRSAATVLAAMKQYCS 435
DB 432 FNVRYVDDEKTNILKYMDPTFRYITRAKAGSKVLVHCKGVGSRSAATVLAAMKQYCS 491
QY 436 LEQALREVOELRPIARNPGLRLOLYOGILTSR-----QSHWEOKVGQVSP 485
DB 492 FOQLEHVKKRSCTIKNKVFLNOLRYSGMLDMKMKELQSKSTTNKSKTADALRP 551
QY 486 EHPAPFV-----STFPPLPEPEGGEKGVWMESSQAAPPEEPFRINLKG 536
DB 552 GSEFTPLIQNLQAKSKSTGAVTPD---GEEBDGSRMRBRRIAQSKQ-----RMM 600
QY 537 VMSGISLPEPLESSETSMDPVEVSSHSSHEEP 573

Db 601 VERSSSTPKTQTAVTVKQOSQSMENLTPESSVAEPP 637

RESULT 14

Q9NV45 PRELIMINARY; PRT; 141 AA.
 ID Q9NV45
 AC Q9NV45
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ10928.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovarian carcinoma;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
 RA Tanai H., Kimata M., Matanabe M., Hirooka S., Ishii S., Kawai Y.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K.,
 RA Masuo Y., Kanehori K.;
 RT "NEBO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK001790; BAA91913.1; -
 DR HSSP; P51452; 1VR.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 DE Hypothetical protein.
 SK SEQUENCE 141 AA; 16357 MW; 5B268790931C5B6 CRC64;

Query Match 17.0%; Score 581.5; DB 4; Length 141;
 Best Local Similarity 89.0%; Pred. No. 1.5e-34;
 Matches 113; Conservative 2; Mismatches 5; Indels 7; Gaps 1;

QY 350 LQNRVTHLN-----MAREINDYPERFTYHNVRLMDEBSAQLPHMKETRFIFAA 402
 Db 13 LSQHPSTILNSSPASHSPMARIDNIFYPERFTYHNVRLMDEBSAQLPHMKETRFIFAA 72
 QY 403 RAQGTHTLVHCKMGVSRSAATVLAAYMKQYCSLEQALRHVOELRPPIARPNGFLRQLOI 462
 Db 73 RAQGTHTLVHCKMGVSRSAATVLAAYMKQYCSLEQALRHVOELRPPIARPNGFLRQLOI 132
 QY 463 YQGILTA 469
 Db 133 YQGILTA 139

RESULT 15

Q9P2P8 PRELIMINARY; PRT; 738 AA.
 ID Q9P2P8
 AC Q9P2P8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein KIAA1298 (Fragment).
 GN KIAA1298.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.XVI.
 The complete sequences of 150 new cDNA clones from brain which code

RT for large proteins in vitro."

RL DNA Ref. 7:65-73(2000).
 DR EMBL; AB037719; BAA92536.1; -
 DR HSSP; Q16828; 1MKP.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 DE Hypothetical protein.
 SK NON TER
 SQ SEQUENCE 738 AA; 80784 MW; C92D75671A510F8A CRC64;

Query Match 12.2%; Score 416.5; DB 4; Length 738;
 Best Local Similarity 36.4%; Pred. No. 1.3e-21;
 Matches 106; Conservative 37; Mismatches 85; Indels 63; Gaps 11;

QY 337 YLG-SENNANLELQNRVTHLNAREINDNIFYPERFTYHNVRLMDEBSAQLPHMKET 395
 Db 5 YLWDRMTSPPLSSIIPIISVDYILNVTREIDNFFPGLFAYHNIRVYDEETDILAHWNEA 64
 QY 396 HRFTEARAQGTHTLVHCKMGVSRSAATVLAAYMKQYCSLEQALRHVOELRPPIARPNG 455
 Db 65 YHFINAKRHSKCLVHCKMGVSRSAATVLAAYMKQYCSLEQALRHVOELRPPIARPNG 124
 QY 456 FLRQLOIYQGITLRASH--VWEQYVG--VSPEEHPA-----EVSTPF- 497
 Db 125 FMRLSEYEGILDASKQHNKLRQOTDSLQFPVDDPAGDPFLPETPGTGESQLPFL 184
 QY 498 -----PPLP-----PEPGGGEKYGVEE-----SQAPKEE--- 525
 Db 185 DDAAGPGLSPPLPCCRRRLSDPLLPSPEDTG--SLVHLEDEPRLALEEAPPAEVR 241
 QY 526 GGPRLRLNGVRSISLEPSL--ELESTSETSDMPVEFSSSHSEHEPL 574
 Db 242 PARQPQ-----QGSLCEKDVKKLEFESPPGRGSLQVETETREBSL 285

Search completed: January 15, 2004, 06:49:23
 Job time : 44 secs

FT Modified-site /note= "O-phosphorylated"
 FT 266 /note= "O-phosphorylated"
 FT Modified-site 286 /note= "O-phosphorylated"
 FT Modified-site 292 /note= "O-phosphorylated"
 FT Modified-site 292 /note= "O-phosphorylated"
 FT Modified-site 484 /note= "O-phosphorylated"
 FT Modified-site 542 /note= "O-phosphorylated"
 FT Modified-site 552 /note= "O-phosphorylated"
 FT Modified-site 564 /note= "O-phosphorylated"
 FT Modified-site 568 /note= "O-phosphorylated"
 FT Modified-site 569 /note= "O-phosphorylated"
 FT Modified-site 649 /note= "O-phosphorylated"
 FT Modified-site 653 /note= "O-phosphorylated"
 FT Modified-site 653 /note= "O-phosphorylated"
 FT Modified-site 65 /note= "O-phosphorylated"
 FT Modified-site 234 /note= "O-phosphorylated"
 FT Modified-site 395 /note= "O-phosphorylated"
 FT Modified-site 638 /note= "O-phosphorylated"
 FT Modified-site 369 /note= "O-phosphorylated"
 FT Modified-site 615 /note= "O-phosphorylated"
 FT Modified-site /note= "N-glycosylated"
 PN WO200120004-A2.
 PD 22-MAR-2001.
 PF 14-SEP-2000; 2000WO-US25515.
 XX 15-SEP-1999; 99US-0154141.
 PR (INCY-) INCYTE GENOMICS INC.
 PA Yue H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y,
 PI Lu DAM;
 XX WPI; 2001-244811/25.
 DR N-PSDB; AAF30485.
 XX
 PT Novel human protein phosphatase and kinase proteins for diagnosis,
 PT treatment and prevention of gastrointestinal, immune system,
 PT neurological and cell proliferative disorders -
 PS Claim 1; Page 93-94; 103pp; English.
 XX
 CC The present sequence is that of novel human protein phosphatase and
 CC kinase protein PPHKP-10, as predicted from Incyte Clone ID No.
 CC 5039718CB1 (see AAF30485). Tissues that express PPHKP-10 (as a
 CC fraction of total tissues expressing PPHKP-10) include reproductive
 CC (0.343), gastrointestinal (0.194) and haematopoietic or immune
 CC (0.134). Diseases or conditions associated with tissues expressing
 CC PPHKP-10 (as a fraction of total tissues expressing PPHKP-10)
 CC include cancer (0.552), inflammation or trauma (0.314) or cell
 CC proliferation (0.090). The encoded protein shows homology to
 CC Drosophila melanogaster Map kinase phosphatase. The invention
 CC provides human PPHKP-1 to -11 polypeptides (see AAB20322-32) and
 CC polynucleotides (see AAF30476-86). It also provides expression
 CC vectors, host cells, antibodies, agonists and antagonists, as well
 CC as methods for diagnosing, treating or preventing disorders
 CC associated with expression of PPHKP, including gastrointestinal

CC disorders, immune system disorders, neurological disorders and cell
 CC proliferative disorders, including cancer.
 XX
 SQ Sequence 659 AA;
 Query Match 100.0%; Score 3412; DB 22; Length 659;
 Best Local Similarity 100.0%; Pred. No. 1e-281;
 Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALVTVSRSPPGSGASTVGPMDQAVQRRSRQRRQSFVLRGAVLQDGGNDDAEA 60
 DB 1 MALVTVSRSPPGSGASTVGPMDQAVQRRSRQRRQSFVLRGAVLQDGGNDDAEA 60
 QY 61 SSEPTEKAPSEBEHLGDDTDPGQSGSPQKQEBQRCHLMVQLRPDDIRLAQLAP 120
 DB 61 SSEPTEKAPSEBEHLGDDTDPGQSGSPQKQEBQRCHLMVQLRPDDIRLAQLAP 120
 QY 121 RPPRLRYLVVSTRREGLSODETVLGVDPDPDSSPSCCTGLVPLMSDTQVYLDGSG 180
 DB 121 RPPRLRYLVVSTRREGLSODETVLGVDPDPDSSPSCCTGLVPLMSDTQVYLDGSG 180
 QY 181 FSVTSGGQSRIFKPISIGTMMATLVHQAEEALGSLVPGSALTWASHYQRLNSEQ 240
 DB 181 FSVTSGGQSRIFKPISIGTMMATLVHQAEEALGSLVPGSALTWASHYQRLNSEQ 240
 QY 241 SCINEMTMADLESIRPPSARPGSSSEQOMEQAIRAMKVLVDSLESTSKERQAL 300
 DB 241 SCINEMTMADLESIRPPSARPGSSSEQOMEQAIRAMKVLVDSLESTSKERQAL 300
 QY 301 ELRLGLPLQOYRDFIDNMLLVAAQRDRASRIFFHLYLGSEWMAANEELQRNVTILN 360
 DB 301 ELRLGLPLQOYRDFIDNMLLVAAQRDRASRIFFHLYLGSEWMAANEELQRNVTILN 360
 QY 361 MAREIDNYPFRFYTHNRLWDEBSAQLFWKTKTHRTLEAARQGHVAVHCKMGYSRS 420
 DB 361 MAREIDNYPFRFYTHNRLWDEBSAQLFWKTKTHRTLEAARQGHVAVHCKMGYSRS 420
 QY 421 AATVLAAYMKQYECGLEQALRHVOELRPIARPNGFLRQLOIYQIGILTASQSHVEKV 480
 DB 421 AATVLAAYMKQYECGLEQALRHVOELRPIARPNGFLRQLOIYQIGILTASQSHVEKV 480
 QY 481 GGVSPDEHPAPREVSTPPPLPPEPBGGEKVYQWESQAAPKXEPGRPRINRGVRS 540
 DB 481 GGVSPDEHPAPREVSTPPPLPPEPBGGEKVYQWESQAAPKXEPGRPRINRGVRS 540
 QY 541 ISLSPSLSTSTSTSMPEVFSHESHEPIQPFQRLARTGGQGVDPDGPALXSR 600
 DB 541 ISLSPSLSTSTSTSMPEVFSHESHEPIQPFQRLARTGGQGVDPDGPALXSR 600
 QY 601 QSVVTLLQGSAAVAVNTOAFQEOEGQGGQGPICISSTPRFRKVVRAQSVHDSGEBGA 659
 DB 601 QSVVTLLQGSAAVAVNTOAFQEOEGQGGQGPICISSTPRFRKVVRAQSVHDSGEBGA 659
 RESULT 2
 ID AAE22729
 AC AAE22729;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Human dual-specificity phosphatase 15 (DSP-15) protein.
 XX
 KW Human; dual-specificity phosphatase 15; DSP-15; anti-allergic; cytostatic;
 KW immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;
 KW signal transduction; cell proliferation; Duchenne muscular dystrophy;
 KW cell cycle abnormality; graft-versus-host disease; autoimmune disease;
 KW metabolic disease; allergy; screening; chromosome 11q.
 XX
 OS Homo sapiens.
 XX
 PN WO200224740-A2.

XX 28-MAR-2002.
 PD
 XX
 PF 19-SEP-2001; 2001WO-US29406.
 XX
 PR 19-SEP-2000; 2000US-23833P.
 PR 18-SEP-2001; 2001US-0955732.
 XX
 PA (CEPT-) CEPTYR INC.
 PI Luche RM, Wei B;
 XX
 DR MPI; 2002-394127/42.
 DR N-PSDB; AAD36061.
 XX
 PT New dual-specificity phosphatase 15 polypeptide and polynucleotides,
 PT useful for treating e.g. Duchenne muscular dystrophy, cancer,
 PT graft-versus-host disease, autoimmune diseases, allergies, metabolic
 PT diseases
 XX
 PS Claim 1, Fig 2; 91pp; English.
 XX
 CC The invention relates to a new isolated dual-specificity phosphatase 15
 CC (DSP-15) polypeptide which retains the ability to dephosphorylate an
 CC activated MAP (mitogen activated protein) kinase. DSPs are phosphatases
 CC that dephosphorylate both phosphotyrosine and phosphothreonine/serine
 CC residues. DSP-15 polypeptide may be used to identify agents that
 CC modulate DSP-15 activity, where such agents may inhibit or enhance signal
 CC transduction via a MAP-kinase cascade, leading to cell proliferation. DSP
 CC polypeptides, modulating agents, and/or polynucleotides encoding the
 CC polypeptides may be used to modulate DSP-15 activity in a patient, and to
 CC ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft-
 CC versus-host disease, autoimmune diseases, allergies, metabolic diseases,
 CC abnormal cell growth, abnormal cell proliferation and cell cycle
 CC abnormalities. DSP-15 alternate form polypeptides are useful in screening
 CC assays for modulators of enzyme activity and/or substrate binding. The
 CC present sequence is human DSP-15 protein. Human DSP-15 gene is located on
 CC chromosome 11q.
 XX
 SQ Sequence 659 AA;
 Query Match 100.0%; Score 3412; DB 23; Length 659;
 Best Local Similarity 100.0%; Pred. No. 1e-281;
 Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTYRSRSPGSGASTPVGPMDOAYORRSRLQRQSFATLRGAVLGLDGGNDAAHA 60
 DB 1 MALVTYRSRSPGSGASTPVGPMDOAYORRSRLQRQSFATLRGAVLGLDGGNDAAHA 60
 QY 61 SSEPTKAPSEELHGDQDFGQGSOPKQESQRLHLMVQLRPDDIRLAQLAP 120
 DB 61 SSEPTKAPSEELHGDQDFGQGSOPKQESQRLHLMVQLRPDDIRLAQLAP 120
 QY 61 SSEPTKAPSEELHGDQDFGQGSOPKQESQRLHLMVQLRPDDIRLAQLAP 120
 DB 61 SSEPTKAPSEELHGDQDFGQGSOPKQESQRLHLMVQLRPDDIRLAQLAP 120
 QY 121 RPRRLRLVSTRREGGLSQDFTVLIGVDFPPSSPSCTLGLVPLMSDTQYYLDGCG 180
 DB 121 RPRRLRLVSTRREGGLSQDFTVLIGVDFPPSSPSCTLGLVPLMSDTQYYLDGCG 180
 QY 121 RPRRLRLVSTRREGGLSQDFTVLIGVDFPPSSPSCTLGLVPLMSDTQYYLDGCG 180
 DB 121 RPRRLRLVSTRREGGLSQDFTVLIGVDFPPSSPSCTLGLVPLMSDTQYYLDGCG 180
 QY 181 FSTVSGGOSRIFPKISIQIWTATLQVYLHQAACALSGVLPSSALTMASHOERLNSBO 240
 DB 181 FSTVSGGOSRIFPKISIQIWTATLQVYLHQAACALSGVLPSSALTMASHOERLNSBO 240
 QY 181 FSTVSGGOSRIFPKISIQIWTATLQVYLHQAACALSGVLPSSALTMASHOERLNSBO 240
 DB 181 FSTVSGGOSRIFPKISIQIWTATLQVYLHQAACALSGVLPSSALTMASHOERLNSBO 240
 QY 241 SCINEMTAMADLESLRPPSAEPGSGSEEQEOMCAIRIAELMKVLDVDSVTSKEIRQAL 300
 DB 241 SCINEMTAMADLESLRPPSAEPGSGSEEQEOMCAIRIAELMKVLDVDSVTSKEIRQAL 300
 QY 241 SCINEMTAMADLESLRPPSAEPGSGSEEQEOMCAIRIAELMKVLDVDSVTSKEIRQAL 300
 DB 241 SCINEMTAMADLESLRPPSAEPGSGSEEQEOMCAIRIAELMKVLDVDSVTSKEIRQAL 300
 QY 301 ELRLGLPLOQYRPFIDNOMLLVAQRDRASRIFFPHLYLGSNNAAVLELQNRVTHILN 360
 DB 301 ELRLGLPLOQYRPFIDNOMLLVAQRDRASRIFFPHLYLGSNNAAVLELQNRVTHILN 360
 QY 301 ELRLGLPLOQYRPFIDNOMLLVAQRDRASRIFFPHLYLGSNNAAVLELQNRVTHILN 360
 DB 301 ELRLGLPLOQYRPFIDNOMLLVAQRDRASRIFFPHLYLGSNNAAVLELQNRVTHILN 360
 QY 361 MAREINDYPERFTYANVRIMDESAQLLPHMKETRFTEAARQGTHTLVACKMGVSRS 420
 DB 361 MAREINDYPERFTYANVRIMDESAQLLPHMKETRFTEAARQGTHTLVACKMGVSRS 420

QY 421 AATVLAAMKQYECSEALRHHVQELRIAPBNPFLQLOIYQILTPASSQSHWEQKV 480
 DB 421 AATVLAAMKQYECSEALRHHVQELRIAPBNPFLQLOIYQILTPASSQSHWEQKV 480
 QY 481 GGVSPEEHPAPVSTPFPPLPPEPGGGEKVWGHEQAAPKEPPGRPRINLAGVRS 540
 DB 481 GGVSPEEHPAPVSTPFPPLPPEPGGGEKVWGHEQAAPKEPPGRPRINLAGVRS 540
 QY 541 ISLLEPSLESTSESDMPVEVSSSHSHEEPLQFPQALRTKGGQOVDRGPPALKSR 600
 DB 541 ISLLEPSLESTSESDMPVEVSSSHSHEEPLQFPQALRTKGGQOVDRGPPALKSR 600
 QY 601 QSVVTLQGSAYVANNTQAFQEOEGQGGGQGPCTISIPRRKRYRQASVHDSGEGEA 659
 DB 601 QSVVTLQGSAYVANNTQAFQEOEGQGGGQGPCTISIPRRKRYRQASVHDSGEGEA 659

RESULT 3
 ABP51654
 ID ABP51654 standard; Protein; 659 AA.
 XX
 AC ABP51654;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human MAP kinase phosphatase splice form 2 protein SEQ ID NO:5.
 XX
 KW Human; phosphatase; mitogen activated protein kinase phosphatase;
 KW MAP kinase; enzyme; chromosome 11.
 OS Homo sapiens.
 XX
 PN WO200242436-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 07-NOV-2001; 2001WO-US42995.
 XX
 PR 20-NOV-2000; 2000US-0725177.
 PR 18-0AN-2001; 2001US-0761640.
 XX
 PA (PEKE) PE CORP NY.
 PI Wei M, Ketchum KA, Di Francesco V, Beasley EM;
 DR N-PSDB; ABQ73250.
 XX
 PT Novel isolated human phosphatase peptide useful for treating disorder
 PT characterized by absence of, inappropriate or unwanted expression of
 PT the phosphatase protein, and as immunogens to raise antibodies
 PS Claim 1; Fig 2A; 85pp; English.
 XX
 CC The present invention describes an isolated human phosphatase peptide
 CC (I). (I) can be used for identifying a modulator of (I) by contacting
 CC (I) with an agent and determining if the agent has modulated the
 CC function or activity of (I). (I) is useful for identifying an agent that
 CC binds to (I), by contacting (I) with an agent and assaying the contacted
 CC mixture to determine whether a complex is formed with the agent bound
 CC (I). The human phosphatases from the present invention are mitogen
 CC activated protein (MAP) kinase phosphatases. These human MAP kinase
 CC phosphatases are located on chromosome 11. (I) and the polynucleotide
 CC sequences encoding (I) can be used in gene therapy. The present sequence
 CC represent human MAP kinase phosphatase splice form 2 from the present
 CC invention.
 XX
 SQ Sequence 659 AA;
 Query Match 99.7%; Score 3402; DB 23; Length 659;
 Best Local Similarity 99.8%; Pred. No. 7.2e-281;
 Matches 658; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALVTASRSPGSGASGAPVGPMPDQAVORRRLQRPSPFAVLGAVLGDGGNDPAEA 60
 DB 1 MALVTASRSPGSGASGAPVGPMPDQAVORRRLQRPSPFAVLGAVLGDGGNDPAEA 60
 QY 61 SSEPTKAPSEEEHIGDQDFGQSGSPQXQEFQRHLHMLVOLLEPPDDIRLAOLEAP 120
 DB 61 SSEPTKAPSEEEHIGDQDFGQSGSPQXQEFQRHLHMLVOLLEPPDDIRLAOLEAP 120
 QY 121 RPRRLRLVAVSRREGGSSODETAVLLGVDFPSSSPCTGLAVLPLMSPTQVYLLDGGG 180
 DB 121 RPRRLRLVAVSRREGGSSODETAVLLGVDFPSSSPCTGLAVLPLMSPTQVYLLDGGG 180
 QY 181 FSVTSGGQSRIKFKPISIQTMATLQVHQAQCEALGSLVPGSSALTMAHRYORINSQ 240
 DB 181 FSVTSGGQSRIKFKPISIQTMATLQVHQAQCEALGSLVPGSSALTMAHRYORINSQ 240
 QY 241 SCINEMTAMADLESRLPPSAEPGGSSQEQEQAIRLEMKVLVDVDSLSVSKETROL 300
 DB 241 SCINEMTAMADLESRLPPSAEPGGSSQEQEQAIRLEMKVLVDVDSLSVSKETROL 300
 QY 301 ELRLGLPQQYRDEIDNQMLLVAQRDRASRIPEPHYLGEEMNAULBEIORRVTHILN 360
 DB 301 ELRLGLPQQYRDEIDNQMLLVAQRDRASRIPEPHYLGEEMNAULBEIORRVTHILN 360
 QY 361 MAREIDNYPREFRYENVRIMDEBSAQLPHMKETHRFIAAQAQSTHVLVHCKMVSRS 420
 DB 361 MAREIDNYPREFRYENVRIMDEBSAQLPHMKETHRFIAAQAQSTHVLVHCKMVSRS 420
 QY 421 AATVLAAMKQYECSEALRHVQELRPIARPNGPFRQIQIGLITASRQSHWECKY 480
 DB 421 AATVLAAMKQYECSEALRHVQELRPIARPNGPFRQIQIGLITASRQSHWECKY 480
 QY 481 GGVSPDEHPAPEVSTPPPLPPEPEEGGEEKVVMESQAAPYEBGPPRINLRGVMRS 540
 DB 481 GGVSPDEHPAPEVSTPPPLPPEPEEGGEEKVVMESQAAPYEBGPPRINLRGVMRS 540
 QY 541 ISLLEPBLEESTSETDMEVPSHSHSEEPLOPPOLARFGQGVDRGQPALKSR 600
 DB 541 ISLLEPBLEESTSETDMEVPSHSHSEEPLOPPOLARFGQGVDRGQPALKSR 600
 QY 601 QSVVTLGSAVAVNARLQAFQEOEGQGGQCEPCISSTPRFRKVRQASVHDSGECEA 659
 DB 601 QSVVTLGSAVAVNARLQAFQEOEGQGGQCEPCISSTPRFRKVRQASVHDSGECEA 659

RESULT 4
 ABB07845 ID ABB07845 standard; Protein: 779 AA.
 XX AC ABB07845;
 XX 03-JUL-2002 (first entry)
 DE Human MAP kinase phosphatase-1-like enzyme.
 XX Mitogen activated protein; MAP; MAP kinase phosphatase-1-like enzyme;
 XX antidiabetic; anorectic; cytosolic; cardiac; human;
 XX antiparkinsonian; cerebroprotective; neuroprotective; nootropic;
 XX neuroleptic; anticonvulsant; anti-HIV; antiarrhythmic; hypotensive;
 XX antiallergic; dermatological; veterinary; gene therapy.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 53 /note= "the encoding codon is not indicated in the
 FT corresponding DNA sequence"
 FT Misc-difference 62 /note= "the encoding codon is not indicated in the
 FT corresponding DNA sequence"
 FT Misc-difference 141 /note= "the encoding codon is not indicated in the
 FT corresponding DNA sequence"

FT Misc-difference 403 /note= "the encoding codon is not indicated in the
 FT corresponding DNA sequence"
 FT Misc-difference 701 /note= "the encoding codon is not indicated in the
 FT corresponding DNA sequence; Xaa can be any
 FT amino acid"
 FT WO200220732-A2.
 PD 14-MAR-2002.
 PR 27-AUG-2001; 2001WO-EP09848.
 PR 07-SEP-2000; 2000US-230709P.
 PA (FARB) BAYER AG.
 PI Liou J;
 DR WPI; 2002-339802/37.
 DR N-PSDB; ABL40805.
 PT New human mitogen activated protein kinase phosphatase-1-like enzyme
 PT polypeptide, regulators of which are useful for preventing, treating
 PT allergies including asthma, diabetes, obesity, cancer and
 PT cardiovascular diseases
 PS Claim 18; Fig 14; 134p; English.
 XX The invention relates to a purified human mitogen activated protein (MAP)
 XX kinase phosphatase-1-like enzyme polypeptide. The enzyme can be expressed
 XX by standard recombinant methodology. The MAP kinase phosphatase-1-like
 XX enzyme and encoding polynucleotides are useful for screening for
 XX modulators which are used for treating a MAP kinase phosphatase-1-like
 XX enzyme dysfunction related disease, such as asthma, a central nervous
 XX system disorder, diabetes, obesity, chronic obstructive pulmonary
 XX disease, cancer or a cardiovascular disease. The enzyme can be regulated
 XX to treat allergies including asthma, allergic rhinitis, atopic
 XX dermatitis, and anaphylaxis, central nervous system disorders such as
 XX brain injuries, Parkinson's disease, dementia, multiple sclerosis,
 XX stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's
 XX disease, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human
 XX immunodeficiency virus (HIV) dementia, and cardiovascular diseases
 XX including myocardial infarction, ischaemic diseases of the heart, atrial
 XX and ventricular arrhythmia, hypertensive vascular diseases and peripheral
 XX vascular diseases. The enzyme is useful in diagnostic assays for
 XX detecting diseases and abnormalities or susceptibility to diseases or
 XX abnormalities related to the presence of mutations in the encoding
 XX nucleic acid sequences. The present sequence represents the human MAP
 XX kinase phosphatase-1-like enzyme polypeptide.
 SO Sequence 779 AA;
 Query Match 83.9%; Score 2863; DB 23; Length 779;
 Best Local Similarity 84.6%; Pred. No. 8,4e-25;
 Matches 581; Conservative 19; Mismatches 39; Indels 48; Gaps 11;
 QY 9 SPPGSGASTPV-GP-----MDQAVQRRSRRLQRPSPFAVL---ALRCSG 79
 DB 24 APVAAAGATLALMGPIIPERGGTALPLVLTALGLLSRQRLVQRRSRRLQRR---ALRCSG 79
 QY 43 GAVLGLQGGNDDAEAASSEPTEKAPSEEEHIGDQDFG-QSGSPQXQEFQRHLHMLVOLLEPPDDIRLAOLEAP 100
 DB 80 GAVLGLQGGNDDAEAASSEPTEKAPSEEEHIGDQDFGCKDPRVRSRSGSNCNL 139
 QY 101 MYQGLRPPDDIRLAOLEA-----PRPRRLRY-LLVASTREGGSLQDETVL-----LGVD 150
 DB 140 MY---RRABAACTSDLAQAAGTGPGLPGRILPCLVSTRGR---RSEPRMRSSWVD 193
 QY 151 FPDSSSPCTGLAVLPLMSDTQVYLDGGGFSVTSGGQSRIKFKPISIQTMATLQVHQA 210
 DB 194 FPDSSSPCTGLAVLPLMSDTQVYLDGGGFSVTSGGQSRIKFKPISIQTMATLQVHQA 253

QY 211 CEALGSGLVPGSGALTWASHYQERLNSSEOSCLNEMWTAMDLSEIRPPSAEPGSGSEQ 270
 Db 254 CEALGSGLVPGSGALTWASHYQERLNSSEOSCLNEMWTAMDLSEIRPPSAEPGSGSEQ 313
 QY 271 MEQAIRAELKVLVDVDSLETSKELRQALELGLPLQGYRDPFINOMLLVAQRDRAS 330
 Db 314 MERAIRAELKVLVDVDSLETSKELRQALELGLPLQGYRDPFINOMLLVAQRDRAS 373
 QY 331 RIFPHLYLGSSEMANANIEELQRNVTHILMAREINDFYERTYNNVRLMDESAQLLP 390
 Db 374 RIFPHLYLGSSEMANANIEELQRNVTHILMAREINDFYERTYNNVRLMDESAQLLP 433
 QY 391 HMKETHRFIABAARQGHVVLVHCKMGVRSAAITVLAAMQYCSLEQALRHVQELRP 450
 Db 434 HMKETHRFIABAARQGHVVLVHCKMGVRSAAITVLAAMQYCSLEQALRHVQELRP 493
 QY 451 RPNPGLRQQLIYQGITLTSRQSHWQKVGVSPBEHPAPEVSTPPPLPPEPGGGE 510
 Db 494 RPNPGLRQQLIYQGITLTSRQSHWQKVGVSPBEHPAPEVSTPPPLPPEPGGGE 553
 QY 511 KVVGMESQAPEEPPRPRLNLRGMRSISLEESLESTSESDMPVSSHESH 570
 Db 554 KVVGMESQAPEEPPRPRLNLRGMRSISLEESLESTSESDMPVSSHESH 613
 QY 571 EEPLOFPPLQARTKGGQVDRGFPQALKSRQSVYTLQGSANVNRTOAFQEOBQGGGQ 630
 Db 614 EEPLOFPPLQARTKGGQVDRGFPQALKSRQSVYTLQGSANVNRTOAFQEOBQGGGQ 673
 QY 631 GEPCISTPPFRKXVNRQASVHDSGEG 657
 Db 674 GEPCISTPPFRKXVNRQASVHDSGEG 700

RESULT 5
 ABP51653
 ID ABP51653 standard; Protein; 471 AA.
 AC ABP51653;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human MAP kinase phosphatase splice form 1 protein SEQ ID NO.4.
 KW Human; phosphatase; mitogen activated protein kinase phosphatase;
 KM MAP kinase; enzyme; chromosome 11.
 XX
 OS Homo sapiens.
 PN WO200242436-A2.
 PD 30-MAY-2002.
 PF 07-NOV-2001; 2001WO-US42995.
 PR 20-NOV-2000; 2000US-0715177.
 PR 18-JAN-2001; 2001US-0761640.
 PA (PEKE) PE CORP NY.
 PI Wei M, Ketchum KA, Di Francesco V, Beasley EM.
 DR WPI, 2002-575237/61.
 DR N-PSDB; ABQ73249, ABQ73252.
 PT Novel isolated human phosphatase peptide useful for treating disorder
 PT characterized by absence of, inappropriate or unwanted expression of
 PT the phosphatase protein, and as immunogens to raise antibodies -
 XX
 PS Claim 1, Fig 2a, 85pp; English.
 CC The present invention describes an isolated human phosphatase peptide
 CC (I). (I) can be used for identifying a modulator of (I) by contacting

CC (I) with an agent and determining if the agent has modulated the
 CC function or activity of (I). (I) is useful for identifying an agent that
 CC binds to (I), by contacting (I) with an agent and assaying the contacted
 CC mixture to determine whether a complex is formed with the agent bound
 CC (I). The human phosphatases from the present invention are mitogen
 CC activated protein (MAP) kinase phosphatases. These human MAP kinase
 CC phosphatases are located on chromosome 11. (I) and the polynucleotide
 CC sequences encoding (I) can be used in gene therapy. The present sequence
 CC represent human MAP kinase phosphatase splice form 1 from the present
 CC invention.
 XX
 SQ Sequence 471 AA;
 QY Query Match 71.1%; Score 2426; DB 23; Length 471;
 Db Best Local Similarity 100.0%; Pred. No. 7e-198;
 Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTSSRPPGSGASTVGPMDQAVQRRSLQRQSFVLRGAVLGLQDGDNDAAEA 60
 Db 1 MALVTSSRPPGSGASTVGPMDQAVQRRSLQRQSFVLRGAVLGLQDGDNDAAEA 60
 QY 61 SSEPTKAPSEBELHGDQTDGQSGSPQKQEBQROHLMVQLRPDDIRLAQLLEAP 120
 Db 61 SSEPTKAPSEBELHGDQTDGQSGSPQKQEBQROHLMVQLRPDDIRLAQLLEAP 120
 QY 121 RPPRLRYLLVSTREGEGLSODETVLGVDPDSSSPSCTGLVLPMSDTQVYLDGPG 180
 Db 121 RPPRLRYLLVSTREGEGLSODETVLGVDPDSSSPSCTGLVLPMSDTQVYLDGPG 180
 QY 121 RPPRLRYLLVSTREGEGLSODETVLGVDPDSSSPSCTGLVLPMSDTQVYLDGPG 180
 Db 121 RPPRLRYLLVSTREGEGLSODETVLGVDPDSSSPSCTGLVLPMSDTQVYLDGPG 180
 QY 181 FSVTSGGGSRIFKPISIQTMATLQVHLQACEALGSLVPGSGALTWASHYQERLNS 240
 Db 181 FSVTSGGGSRIFKPISIQTMATLQVHLQACEALGSLVPGSGALTWASHYQERLNS 240
 QY 241 SCINEMTMADLESIRPPSAEPGSGSEQOEQAIRALMVLVDVDSLETSKELRQAL 300
 Db 241 SCINEMTMADLESIRPPSAEPGSGSEQOEQAIRALMVLVDVDSLETSKELRQAL 300
 QY 301 EURLGLPLQGYRDPFINOMLLVAQRDRASRIFFHLYLGSSEMANANIEELQRNVTHILN 360
 Db 301 EURLGLPLQGYRDPFINOMLLVAQRDRASRIFFHLYLGSSEMANANIEELQRNVTHILN 360
 QY 361 MAREIDNFPFRFYHNVRLMDEBSAQLLPWKETHRFIEAARQGHVVLVHCKMGVRS 420
 Db 361 MAREIDNFPFRFYHNVRLMDEBSAQLLPWKETHRFIEAARQGHVVLVHCKMGVRS 420
 QY 421 AATVLAAMKQYECSEALRHVOELRPIARNPGFLROLIYQGITLA 469
 Db 421 AATVLAAMKQYECSEALRHVOELRPIARNPGFLROLIYQGITLA 469

RESULT 6
 AAE22733
 ID AAE22733 standard; Protein; 471 AA.
 AC AAE22733;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Murine dual-specificity phosphatase 15 (DSP-15) protein.
 KW Murine; dual-specificity phosphatase 15; DSP15; antiallergic; cytostatic;
 KW immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;
 KW signal transduction; cell proliferation; Duchenne muscular dystrophy;
 KW cell cycle abnormality; graft-versus-host disease; autoimmune disease;
 KW metabolic disease; allergy; screening.
 XX
 OS Mus musculus.
 PN WO200224740-A2.
 PD 28-MAR-2002.
 PR 19-SEP-2001; 2001WO-US29406.

XX 19-SEP-2000; 2000US-233833P.
PR 18-SEP-2001; 2001US-0955732.

XX (CEPT-) CEPTVR INC.

XX Luche RM, Wei B;

XX WPI, 2002-394127/42.

XX N-PSDB; AAD36063.

XX New dual-specificity phosphatase 15 polypeptide and polynucleotides,
PT useful for treating e.g. Duchenne muscular dystrophy, cancer,
PT graft-versus-host disease, autoimmune diseases, allergies, metabolic
PT diseases -

XX Claim 50; Fig 5; 91pp; English.

XX The invention relates to a new isolated dual-specificity phosphatase 15
CC (DSP-15) polypeptide which retains the ability to dephosphorylate an
CC activated MAP (mitogen activated protein) kinase. DSPs are phosphatases
CC that dephosphorylate both phosphotyrosine and phosphothreonine/serine
CC residues. DSP-15 polypeptides may be used to identify agents that
CC modulate DSP-15 activity, where such agents may inhibit or enhance signal
CC transduction via a MAP-kinase cascade, leading to cell proliferation. DSP
CC polypeptides, modulating agents, and/or polynucleotides encoding the
CC polypeptides may be used to modulate DSP-15 activity in a patient, and to
CC ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft-
CC versus-host disease, autoimmune diseases, allergies, metabolic diseases,
CC abnormal cell growth, abnormal cell proliferation and cell cycle
CC abnormalities. DSP-15 alternate form polypeptides are useful in screening
CC assays for modulators of enzyme activity and/or substrate binding. The
CC present sequence is murine DSP-15 protein.

XX Sequence 471 AA;

XX Query Match 71.1%; Score 2426; DB 23; Length 471;

XX Best Local Similarity 100.0%; Pred. No. 7e-198; Mismatches 0; Gaps 0;

XX Matches 469; Conservative 0; Indels 0;

XX 1 MALVTVSRSPPGSGASTPVGPMDOAVORRSLQRSGFAVLRGAVLGLDGGNDADA 60

XX 1 MALVTVSRSPPGSGASTPVGPMDOAVORRSLQRSGFAVLRGAVLGLDGGNDADA 60

XX 61 SSEPTEKAPSEBEELHGDQTFDGGSGSPQKOEORHLMVQLRPQDDIRLAOLEAP 120

XX 61 SSEPTEKAPSEBEELHGDQTFDGGSGSPQKOEORHLMVQLRPQDDIRLAOLEAP 120

XX 121 RPPRLRYLLVSTREGGLSODETVLLGVDPDSSSPSCCTGLVPLMSDTQVYLDGG 180

XX 121 RPPRLRYLLVSTREGGLSODETVLLGVDPDSSSPSCCTGLVPLMSDTQVYLDGG 180

XX 181 FSVTSGGSGSRIFKPISTQTMWATLQVLAHQCEALGSGLVFGSALTWASHYGERLNSQ 240

XX 181 FSVTSGGSGSRIFKPISTQTMWATLQVLAHQCEALGSGLVFGSALTWASHYGERLNSQ 240

XX 241 SCINEMTAMADLESRLPPSAEPGSSSQEOEQAIRAELMKVLDVDSLESTSKERQAL 300

XX 241 SCINEMTAMADLESRLPPSAEPGSSSQEOEQAIRAELMKVLDVDSLESTSKERQAL 300

XX 301 ELRLGLFLQOYRDIQNMQLLVVQRASRIFFPHLVLGSEMNANLELQRRVTHIN 360

XX 301 ELRLGLFLQOYRDIQNMQLLVVQRASRIFFPHLVLGSEMNANLELQRRVTHIN 360

XX 361 MAREIDNFYPERFTYHNVRLWDEBSAQLPHWKETHFIEAARQGTHTLVHCKMGVS 420

XX 361 MAREIDNFYPERFTYHNVRLWDEBSAQLPHWKETHFIEAARQGTHTLVHCKMGVS 420

XX 421 AATYLAAMQYECSTLQALRHVQELAPARPNNGFLROLQIYGILTA 469

XX 421 AATYLAAMQYECSTLQALRHVQELAPARPNNGFLROLQIYGILTA 469

XX 469 AATYLAAMQYECSTLQALRHVQELAPARPNNGFLROLQIYGILTA 469

XX 469 AATYLAAMQYECSTLQALRHVQELAPARPNNGFLROLQIYGILTA 469

RESULT 7
ABP51655
ID ABP51655 standard; Protein; 408 AA.

XX ABP51655;

XX 30-SEP-2002 (first entry)

XX Human MAP kinase phosphatase splice form 3 protein SEQ ID NO:6.

XX Human; phosphatase; mitogen activated protein kinase phosphatase;

XX MAP kinase; enzyme; chromosome 11.

XX Homo sapiens.

XX WO200242436-A2.

XX 30-MAY-2002.

XX 07-NOV-2001; 2001WO-US42995.

XX 20-NOV-2000; 2000US-0715177.

XX 18-JAN-2001; 2001US-0761640.

XX (PEKE) PE CORP NY.

XX Wei M, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-575237/61.

XX N-PSDB; ABQ73255.

XX Novel isolated human phosphatase peptide useful for treating disorder

XX characterized by absence of, inappropriate or unwanted expression of

XX the phosphatase protein, and as immunogens to raise antibodies

XX Claim 1; Fig 2A; 85pp; English.

XX The present invention describes an isolated human phosphatase peptide

XX (I). (I) can be used for identifying a modulator of (I) by contacting

XX (I) with an agent and determining if the agent has modulated the

XX function or activity of (I). (I) is useful for identifying an agent that

XX binds to (I), by contacting (I) with an agent and assaying the contacted

XX mixture to determine whether a complex is formed with the agent bound

XX (I). The human phosphatases from the present invention are mitogen

XX activated protein (MAP) kinase phosphatases. These human MAP kinase

XX phosphatases are located on chromosome 11. (I) and the polynucleotide

XX sequences encoding (I) can be used in gene therapy. The present sequence

XX represent human MAP kinase phosphatase splice form 3 from the present

XX invention.

XX Sequence 408 AA;

XX Query Match 60.1%; Score 2051.5; DB 23; Length 408;

XX Best Local Similarity 86.6%; Pred. No. 4.7e-166; Mismatches 0; Gaps 1;

XX Matches 406; Conservative 0; Indels 63;

XX 1 MALVTVSRSPPGSGASTPVGPMDOAVORRSLQRSGFAVLRGAVLGLDGGNDADA 60

XX 1 MALVTVSRSPPGSGASTPVGPMDOAVORRSLQRSGFAVLRGAVLGLDGGNDADA 60

XX 61 SSEPTEKAPSEBEELHGDQTFDGGSGSPQKOEORHLMVQLRPQDDIRLAOLEAP 120

XX 61 SSEPTEKAPSEBEELHGDQTFDGGSGSPQKOEORHLMVQLRPQDDIRLAOLEAP 120

XX 121 RPPRLRYLLVSTREGGLSODETVLLGVDPDSSSPSCCTGLVPLMSDTQVYLDGG 180

XX 121 RPPRLRYLLVSTREGGLSODETVLLGVDPDSSSPSCCTGLVPLMSDTQVYLDGG 180

XX 181 FSVTSGGSGSRIFKPISTQTMWATLQVLAHQCEALGSGLVFGSALTWASHYGERLNSQ 240

XX 181 FSVTSGGSGSRIFKPISTQTMWATLQVLAHQCEALGSGLVFGSALTWASHYGERLNSQ 240

XX 241 SCINEMTAMADLESRLPPSAEPGSSSQEOEQAIRAELMKVLDVDSLESTSKERQAL 300

XX 241 SCINEMTAMADLESRLPPSAEPGSSSQEOEQAIRAELMKVLDVDSLESTSKERQAL 300

Db 202 -----SEEQMEQALRAELMKVLDVSDLESVTSKEIRQAL 237

QY 301 ERLGLPLQOYRDFIDNOMLLVAQDRASRIFFPHLYGSEWMANLEELQNRVTHILN 360

Db 238 ERLGLPLQOYRDFIDNOMLLVAQDRASRIFFPHLYGSEWMANLEELQNRVTHILN 297

QY 361 MAREIDNFPYPERFTYHNVRMLDEBSAQLLPHWKETHRFIEARAQGTHTLVHCKMGVSRS 420

Db 298 MAREIDNFPYPERFTYHNVRMLDEBSAQLLPHWKETHRFIEARAQGTHTLVHCKMGVSRS 357

QY 421 AATVLAAMKOYECSELOALRHVQELRPPIARPNGFLRQLOIYQGITLA 469

Db 358 AATVLAAMKOYECSELOALRHVQELRPPIARPNGFLRQLOIYQGITLA 406

RESULT 8

AB97419 ID ABB97419 standard; Protein; 394 AA.

AC ABB97419;

XX 27-JUN-2002 (first entry)

DT Novel human protein SEQ ID NO: 687.

DE Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;

KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;

KM neuroprotective; antiparkinsonian; protein therapy; EST;

KX expressed sequence tag.

XX Homo sapiens.

OS WO20022660-A2.

XX 21-MAR-2002.

PD 10-SEP-2001; 2001WO-US26015.

PF 11-SEP-2000; 2000US-0659671.

PR (HYSB-) HYSBQ INC.

XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wenman T, Drmanac RT;

XX N-PSDB; ABN32605.

DR WPI; 2002-292408/33.

XX An isolated polynucleotide for treating diseases associated with its

PT encoded polypeptide such as cancer and multiple sclerosis -

PS Claim 20; SEQ ID NO 687; 509bp; English.

XX The present invention provides the protein and coding sequences of 444

CC novel human proteins. These were isolated from expressed sequences tags

CC (ESTs). They can be used to stimulate cell growth, to regulate

CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

CC e.g. in burn treatment, to regulate the immune system e.g. to treat

CC multiple sclerosis, to regulate activin or inhibin e.g. to treat

CC infertility, to regulate haemostasis or thrombolysis e.g. to treat

CC stroke and cancer, to screen for drugs, to treat inflammatory conditions

CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.

CC Parkinson's disease. The present sequence is a protein of the invention.

XX Sequence 394 AA;

QY Query Match 55.2%; Score 1884.5; DB 23; Length 394;

Best Local Similarity 59.8%; Pred. No. 7.8e-152;

Matches 394; Conservative 0; Mismatches 0; Indels 265; Gaps 1;

QY 1 MALVTYRSRPPGSGASTPVGPMQAVQRRSLQRQSPAVLGVGLDGGDNDAAEA 60

Db 1 MALVTYRSRPPGSGASTPVGPMQAVQRRSLQRQSPAVLGVGLDGGDNDAAEA 60

QY 61 SSEPTEKAPSEELHGGQOTDFGGSSPOKOEORGLHLMVQLRPDDIRLAQLEAP 120

Db 61 SSEPTEKAPSEELHGGQOTDFGGSSPOKOEORGLHLMVQLRPDDIRLAQLEAP 120

QY 121 RPPRLRYLLVSTTEGEGLSQDETIVLLGVDFPDSSSPSCTLGVLPLMSDTQVYLDGCG 180

Db 121 RPPRLRYLLVSTTEGEGLSQDETIVLLGVDFPDSSSPSCTLGVLPLMSDTQVYLDGCG 180

QY 181 FSVTSGGQSRIFKXISITQTMATLQVTHQACEALGSGVLPGGSGALTWASHYQERLNSQ 240

Db 181 FSVTSGGQSRIFKXISITQTMATLQVTHQACEALGSGVLPGGSGALTWASHYQERLNSQ 240

QY 241 SCLENTAMADLESIRPPSAEPGSSSEQOMEQAIRAELMKVLDVSDLESVTSKEIRQAL 300

Db 241 SCLENTAMADLESIRPPSAEPGSSSEQOMEQAIRAELMKVLDVSDLESVTSKEIRQAL 300

QY 301 ERLGLPLQOYRDFIDNOMLLVAQDRASRIFFPHLYGSEWMANLEELQNRVTHILN 360

Db 283 -----

QY 361 MAREIDNFPYPERFTYHNVRMLDEBSAQLLPHWKETHRFIEARAQGTHTLVHCKMGVSRS 420

Db 283 -----

QY 421 AATVLAAMKOYECSELOALRHVQELRPPIARPNGFLRQLOIYQGITLAHQSHWEQKV 480

Db 283 -----

QY 481 GGVSPDEHPAPREVSTPPPLPPEPBGGEKRYVMESQAAPKEBPGRPRINRGVMRS 540

Db 283 -----

QY 541 ISLLEPSLEESTSETSDMPEVFESHSHEEPLOPPOLARTKGQGVNDGPPALAKSR 600

Db 283 -----LELESTSETSDMPEVFESHSHEEPLOPPOLARTKGQGVNDGPPALAKSR 335

QY 601 QSVVTLQGSAAVANKRTAFQEOEGOGGQGPCTISSTPPRRKVRQASVHDSGEDEA 659

Db 336 QSVVTLQGSAAVANKRTAFQEOEGOGGQGPCTISSTPPRRKVRQASVHDSGEDEA 394

RESULT 9

AB973226 ID AAB73226 standard; Protein; 341 AA.

AC AAB73226;

XX 11-MAY-2001 (first entry)

DT Human phosphatase NP_060746_h.

DE Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;

KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;

KM congenital muscle disorder; Papillon-Leleuve syndrome; Cowden disease;

KW Moebius syndrome; Biorstad syndrome; Bannayan Zonana syndrome;

XX schizophrania; hamartoma.

OS Homo sapiens.

XX WO200112819-A2.

PN 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US22158.

PF 13-AUG-1999; 99US-0149005.

PR (SUGB-) SUGEN INC.

XX Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;

DR WPI; 2001-211226/21.
 DR N-PSDB; AAF63578.
 XX New protein phosphatase polypeptide for diagnosing and treating
 PT phosphatase related disorders such as cancer, schizophrenia, cardiac
 PT dysfunction and/or vascular disorders
 XX
 XX Claim 6; Fig 5; 138pp; English.
 XX
 CC The present invention relates to phosphatase proteins and coding
 CC sequences. The present sequence is one such phosphatase. Phosphatases are
 CC enzymes that catalyze the dephosphorylation of proteins modified by
 CC phosphorylation of serine, threonine or tyrosine residues. The
 CC phosphatases are useful for treating a variety of diseases: for example
 CC cancer e.g. breast, uterine, prostate, head, neck, lung cancers,
 CC synovial sarcoma, renal cell carcinoma, non-small cell lung cancer,
 CC hepatocellular carcinoma, pancreatic endocrine tumors, stomach cancer,
 CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological
 CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,
 CC congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease,
 CC ectodermal dysplasia, Moebius syndrome, Bjornsted syndrome, Bannayan
 CC Zonana syndrome, schizophrenia and hamartomas.
 CC
 XX
 SQ Sequence 341 AA;
 Query Match 52.1%; Score 1779; DB 22; Length 341;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-143; Indels 0; Gaps 0;
 Matches 341; Conservative 0; Mismatches 0;
 QY 319 MLILVQQRDRASRIFPHLYGSEMNANLEELQNRVTHILNMAEIDNFPYERFTYANV 378
 DB 1 MLILVQQRDRASRIFPHLYGSEMNANLEELQNRVTHILNMAEIDNFPYERFTYANV 60
 QY 379 RLWDEBSAQLLPWKKEHRIEAAAGCTIVLVHCKMGVSRSAATLAAAMQYEGSLEQ 438
 DB 61 RLWDEBSAQLLPWKKEHRIEAAAGCTIVLVHCKMGVSRSAATLAAAMQYEGSLEQ 120
 QY 439 ALHNVCELRPIARPNPGFLRQLQIYOGILTASRQSHVQKGVSPSEHPAPEVSTPP 498
 DB 121 ALHNVCELRPIARPNPGFLRQLQIYOGILTASRQSHVQKGVSPSEHPAPEVSTPP 180
 QY 499 PLPEPEGGGEEYKVMESQAAPKEBPGRPRINLRGVMSLSLEBLSLESTSETSD 558
 DB 181 PLPEPEGGGEEYKVMESQAAPKEBPGRPRINLRGVMSLSLEBLSLESTSETSD 240
 QY 559 MPEVFSHSHSEHPLOPFPOLARTKGQGVDRGPQALPKRSQSVTTLGSAVVAARQA 618
 DB 241 MPEVFSHSHSEHPLOPFPOLARTKGQGVDRGPQALPKRSQSVTTLGSAVVAARQA 300
 QY 619 FQEOGQGGQGGGEPICISSTPRFRKVVRAQSVHDSGEDEGA 659
 DB 301 FQEOGQGGQGGGEPICISSTPRFRKVVRAQSVHDSGEDEGA 341
 RESULT 10
 ABP51656
 ID ABP51656 standard; Protein: 312 AA.
 XX
 AC ABP51656;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human MAP kinase phosphatase related protein sequence SEQ ID NO:8.
 XX
 KW Human MAP kinase phosphatase; mitogen activated protein kinase phosphatase;
 XX MAP kinase; enzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO200242436-A2.
 XX
 XX 30-MAY-2002.
 XX
 XX

PF 07-NOV-2001; 2001MO-US42995.
 XX
 XX 20-NOV-2000; 2000US-0715177.
 PF 18-JAN-2001; 2001US-0761640.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX
 PI Wei M, Ketchum KA, Di Francesco V, Beasley EM;
 DR WPI; 2002-575237/61.
 XX
 XX Novel isolated human phosphatase peptide useful for treating disorder
 PT characterized by absence of, inappropriate or unwanted expression of
 PT the phosphatase protein, and as immunogens to raise antibodies
 XX
 XX Disclosure; Fig 2C; 85pp; English.
 XX
 CC The present invention describes an isolated human phosphatase peptide
 CC (I). (I) can be used for identifying a modulator of (I) by contacting
 CC (I) with an agent and determining if the agent has modulated the
 CC function or activity of (I). (I) is useful for identifying an agent that
 CC binds to (I), by contacting (I) with an agent and assaying the contacted
 CC mixture to determine whether a complex is formed with the agent bound
 CC (I). The human phosphatases from the present invention are mitogen
 CC activated protein (MAP) kinase phosphatases. These human MAP kinase
 CC phosphatases are located on chromosome 11. (I) and the polynucleotide
 CC sequences encoding (I) can be used in gene therapy. The present sequence
 CC represents a human protein which is given in comparison with a human MAP
 CC kinase phosphatase from the present invention.
 CC
 XX
 SQ Sequence 312 AA;
 Query Match 43.1%; Score 1470.5; DB 23; Length 312;
 Best Local Similarity 92.8%; Pred. No. 1, 1e-116;
 Matches 290; Conservative 6; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MALVTVSRSPPGSGASIPVGMDOAVRRRLRQSGFAVLRGAVYGLQGGNDDBAABA 60
 DB 1 MALVTVSRSPPGSGASIPVGMDOAVRRRLRQSGFAVLRGAVYGLQGGNDDBAABA 60
 QY 61 SSBPTERKAPSEELHGGQTDFGQGSQSPQKQEBQRCHILMVQLRPODDIRLAQLEAP 120
 DB 61 SSBPTERKAPSEELHGGQTDFGQGSQSPQKQEBQRCHILMVQLRPODDIRLAQLEAP 120
 QY 121 RPPRLRYLLVYSTRGEGLSODEFTVLGVDFPDSSSSCTLGLVLPWSTQYVLDGCG 180
 DB 121 RPPRLRYLLVYSTRGEGLSODEFTVLGVDFPDSSSSCTLGLVLPWSTQYVLDGCG 180
 QY 181 FSVTSGGGSRIFFKISIQTMATLQVHQAQCEALGSLVPGSGALTWASHYQERLNSQ 240
 DB 181 FSVTSGGGSRIFFKISIQTMATLQVHQAQCEALGSLVPGSGALTWASHYQERLNSQ 240
 QY 241 SCINEMWTAMDLSELRPASAPGSSSQEQMEQAIRAELMKVLDV-SDLSEVTSKETRQA 299
 DB 241 SCINEMWTAMDLSELRPASAPGSSSQEQMEQAIRAELMKVLESTSETSDMPEVFS 300
 QY 300 LELRLGLPQY 311
 DB 301 HESSHEEPLOP 312
 RESULT 11
 AAE04833
 ID AAE04833 standard; Protein: 1049 AA.
 XX
 AC AAE04833;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human SGP006 phosphatase polypeptide.
 XX
 KW Human; SGP006 phosphatase polypeptide; phosphatase-related disease;
 XX immune-related disorder; ocular disease; organ transplant rejection;
 XX

| | | | | |
|-----------|--|-----|--|-----|
| Oy | | 57 | AABASSEPEPKAPSEEEHLGQTFDGGCS--OSPCKOQ--ECPCHILMLVOLLRPDDIRLA | 114 |
| Dd | | 56 | -----SSPQ-----CGSLQHPIHGAGDLPHQLQWIMINLRCCEDRIKLA | 94 |
| Oy | | 115 | AQLEADPRPLRLYLIV--STREGGLSODETVLLGVDFPDSSSPSCTLGIYLPMSDTQ | 172 |
| Dd | | 95 | VRLSESMAARVMRYVMVVYSGSGRQ---DTEENILLGVDFPSKEKESCTIIGVATRLMWDTK | 150 |
| Oy | | 173 | VVLDEGGGVSIVSGGSGSRIFKPISQTMMATLQVLMHOCFAALSGAVPGGSALTMAHY | 232 |
| Dd | | 151 | IHLDGGGSVSSTAGAMHTFKFVSYQANMSALOULHKACEYARKHNYPFGVALIMATYY | 210 |
| Oy | | 233 | QERLNSEGQCLNEMWTAMLDLESIRD--PSAEFGSSSEQEQMEQAIRALEMKVLDVSDLES | 290 |
| Dd | | 211 | ESCISEEGSCINEMNMAMQDLSTRDPDSPALFYVDKPTGEGERTERLIKAKRSIMMSODLEN | 270 |
| Oy | | 291 | VTSKETROLDELRLGLPQQYNDPFDNQMLLVACRQASRIFPHLYLSGBMNAAINTEL | 350 |
| Dd | | 271 | VTSKETRNELKKOMCNLKELEKFTIDNMLLITLGMDXSLIFPHLYLVSGBMNASNLEEL | 330 |
| Oy | | 351 | QNRNRVTHLINMARIEDINPFPERFTYANVLMDEESAOLPHMKETHRFEINARAOGTHVL | 410 |
| Dd | | 331 | QSGGVAYILNVTRIEDINFPDGLFAAHNIKVYDEETDLLAHMNAEYHFINKAKNHSEKCL | 390 |
| Oy | | 411 | VHCKMVGVSASATVLAIVANKQYECGLEQALHHVCDELPIRAPNNGFLROLQIYGILITAS | 470 |
| Dd | | 391 | VHCKMVGVSASATVLAIVANKREGMPELEXAIVYVKOKSLTTPNAGFMKOLEYEGLIDAS | 450 |
| Oy | | 471 | ROSH--VWEPOKVG--VSPREEHPA-----PEVATPE-----PPLP-- | 501 |
| Dd | | 451 | KORHAKMLMQQDSSLSIQPVDPAPRGPILETPTGRTESQLPFLDDAAGLGPPLPCC | 510 |
| Oy | | 502 | -----DEPEGGEEKVYGNES-----SQAAPKEE--PGDRPRINIRGVMS | 540 |
| Dd | | 511 | FRLSLDPLLPSPEDERG--SLVHLEDPERALLLEAPPAEVHARPAPQP-----QG | 560 |
| Oy | | 541 | ISLLEPSL--ELESTSETSDMEFVSSHSHSHEEPL | 574 |
| Dd | | 561 | SGLCERDVKKKLFFGSPKRGSSCLLQVETERBESL | 596 |
| <hr/> | | | | |
| RESULT 12 | | | | |
| AAE04835 | | | | |
| ID | AAE04835 standard; Protein; 498 AA. | | | |
| XX | | | | |
| AC | AAE04835; | | | |
| XX | | | | |
| DT | 10-SEP-2001 (first entry) | | | |
| XX | | | | |
| DE | Human GSP001 phosphatase polypeptide. | | | |
| XX | | | | |
| KW | Human; GSP001 phosphatase polypeptide; phosphatase-related disease; | | | |
| KW | immune-related disorder; ocular disease; organ transplant rejection; | | | |
| KW | infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; | | | |
| KW | metabolic disorder; haematopoietic cancer; mood disorder; cardiac; | | | |
| KW | Parkinson's disease; multiple sclerosis; amotrophic lateral sclerosis; | | | |
| KW | cardiovascular disease; brain; neuronal-associated disease; dysostosis; | | | |
| KW | attention disorder; cognition disorder; noctropic; psychotic disorder; cyrostatic; | | | |
| KW | neurological disorder; virutide; nocotropic; cerebroprotective; therapy; | | | |
| KW | neuroprotective; antibacterial; antineoplastic; transquilliser; antistematic; | | | |
| KW | hypotensive; immunosuppressive; antiaporiatic; analgesic; hypertensive; | | | |
| KW | antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase; | | | |
| KW | MRP; migraine; chromosome Xg11.1-11.3. | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| Key | Location/Qualifiers | | | |
| FT | 1..173 | | | |
| FT | Domain | | | |
| FT | /label= Catalytic_domain | | | |
| FT | 307..441 | | | |
| FT | Domain | | | |
| FT | /label= Phosphatase_domain | | | |
| XX | | | | |
| FN | W0200146394-A2. | | | |

| | | | |
|--|---|--|--|
| Pd | | 28-JUN-2001. | |
| Pf | | | |
| Xx | | 21-DEC-2000; 2000NO-US34736. | |
| Xx | | | |
| Ff | | 21-DEC-1999; 99US-0173255. | |
| Ff | | 28-DEC-1999; 99US-0175766. | |
| Ff | | 25-JAN-2000; 2000US-0178078. | |
| Ff | | 31-JAN-2000; 2000US-0179301. | |
| Xx | | (SUGF-) SUGEN INC. | |
| Pa | | | |
| Xx | | Plowman GD, Martinez R, Whyte D, Manning G, Sudarsanam S, Hill RJ, | |
| Ff | | Flanagan P; | |
| Xx | | WPI; 2001-418058/44. | |
| Df | | N-PSDB; AAD09493. | |
| Pt | | | |
| Pt | | Novel phosphatase polypeptide useful for treating cancers, | |
| Pt | | immune-related diseases and disorders, cardiovascular disease, brain or | |
| Pt | | neural-associated diseases and metabolic disorders | |
| Xx | | | |
| Pf | | Claim 7; Fig 2; 186pp; English. | |
| Xx | | | |
| Cc | | The present invention relates to phosphatase polypeptides, nucleotide | |
| Cc | | sequences encoding them, as well as various products and methods useful | |
| Cc | | for the diagnosis and treatment of various phosphatase-related diseases | |
| Cc | | and conditions. Substance that modulates the activity of phosphatase | |
| Cc | | polypeptide is used to treat immune-related diseases and disorders, | |
| Cc | | cardiovascular disease, brain or neural-associated diseases and | |
| Cc | | metabolic disorders, including cancers of tissues, cancers of | |
| Cc | | haematopoietic origin, diseases of central and peripheral nervous | |
| Cc | | system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, | |
| Cc | | amyotrophic lateral sclerosis, viral infections, infections caused by | |
| Cc | | prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain, | |
| Cc | | sexual dysfunction, mood disorders, attention disorders, cognition | |
| Cc | | disorders, hypertension, hyperextension, psychotic disorders, neurological | |
| Cc | | disorders, dyskinesias and organ transplant rejection. The present | |
| Cc | | amino acid sequence is human SG001 phosphatase polypeptide. This | |
| Cc | | sequence is classified as dual specificity phosphatase (DSP) and MAP | |
| Cc | | kinase phosphatase (MKP). SG001 gene maps to chromosomal position | |
| Cc | | Xp11.1-11.3. | |
| Cc | | | |
| Sq | Sequence | 498 AA; | |
| Xx | | | |
| Query Match | 31.9%; Score 1089.5; DB 22; Length 498; | | |
| Best Local Similarity | 42.1%; Pred. No. 6-7e-84; | | |
| Matches 227; Conservative 102; Mismatches 149; Indels 61; Gaps 9 | | | |
| Oy | 1 MALVTVRSRSPGSGASTPVGPWDQAVRRSRIGQR--QSFAVLRGAVLGLDGGNDGA 57 | | |
| Df | 1 MAALVTQVRSPPTPTSTSSPCASPADSGEEBCRSQPRISSEFLTKYKGAALPLRP----- 53 | | |
| Oy | 58 AAASSEPTEKAPEEELHGDQDFPGSGSSPOKDEO-----ROTHLMVOQLRPDD 110 | | |
| Df | 54 -----GNGSTRIRSHRKAKAGDLQTLQGMPLRLPEDN 89 | | |
| Oy | 111 IRLAQLEAPRPRLRYLLVSTREGEGLSODETVLLGVDPDSSSPCTLGLVLPMSD 170 | | |
| Df | 90 IRLAVERLESTYQNRRTMYVVVSTNGRQ--DIIEESTIVLGMPSSSDSTCTMGILPLMSD 147 | | |
| Oy | 171 TOYVLDGGDGFSVTSQSGGRIFKPISITOMATLTQVHQAEALMGLSVPGSGALTWMS 230 | | |
| Df | 148 TLHLHDGGGFVSISTNRVHKRFVSQAMNSALOSLKACEVAIRAINYPGSLFTLWS 207 | | |
| Oy | 231 HYGERLNSEGSCINENTAMADELSRP--PSAEPGSGSEDOEQAIRAEIWLVDVSDL 288 | | |
| Df | 208 YESHINSIDSSVENEMNAQDVQSHRPDSPALFTDIPERERTERLTKTFLREIMMQXDL 267 | | |
| Oy | 289 EASYTSKEIQALELRGLPLQCYRPFINOMILLVAQDRASRIFFPLVYGSRMANNE 348 | | |
| Df | 268 ENITSKEIRLETEMQVCNLREFKEFINDEMIVILGQWDSPTQLFEHVFGSEWANSNDE 327 | | |

| | | | | |
|--|--|-----|---|-----|
| CY | | 349 | ELOQRNVTILIMNAEIDNFYEERTYNVNLMBDESQOLLPHKKEHRFLEAARAGCTH | 408 |
| D6 | | 328 | DLDNRGRRIYLANTRRIDNFPDGVFEYRIRKYDEEARIDLAYNDYRKISAKKHGSK | 387 |
| OY | | 409 | VLVHCCKGYSRSAAATVLAYAMKQVECSLEOALRHVOELRPAPDPFLRQIQIGILT | 468 |
| D6 | | 388 | CLVHCCKGYSRSASITLAYAMEKY---DRADVDYKERRTYTKENPSEFMQLERYQGILL | 443 |
| OY | | 469 | ASLQSHWMECKYGKGSPEEHPRAPENVSTPP-----PLPRPDGGEGEKVKVMGESQAP | 522 |
| D6 | | 444 | ASFLGLIHL---GG--RDKPWGKSTEFESVDLYSLGPSGCCNPRLHLISHPIULTP | 495 |
| RESULT 13 AAE06775 AAE06775 standard; Protein, 509 AA. XX AC AAE06775; XX DT 16-OCT-2001 (first entry) XX DE Human dual-specificity phosphatase (DSP)-13 protein. | | | | |
| XX | Human dual-specificity phosphatase; DSP-13; dual phosphorylation motif; | | | |
| KW | Human; dual-specificity phosphatase; DSP-13; dual phosphorylation motif; | | | |
| KW | mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease; | | | |
| KW | GMD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; | | | |
| KW | allergy; metabolic disease; cell growth; cell proliferation; cytostatic; | | | |
| KW | cell cycle abnormality; cell differentiation; antiallergic; muscular; | | | |
| KX | immunosuppressive. | | | |
| OS | Homo sapiens. | | | |
| FH | Key Location/Qualifiers | | | |
| FT | Domain 395..415 | | | |
| FT | /note="Active site domain" | | | |
| FN | WO200157221-A2. | | | |
| PD | 09-AUG-2001. | | | |
| PF | 01-FEB-2001; 2001MO-US03429. | | | |
| PR | 02-FEB-2000; 2000US-0179886. | | | |
| PA | (CEPT-) CEPTYR INC. | | | |
| PI | Luche RM, Wei B; | | | |
| PI | WP1: 2001-488887/53. | | | |
| DR | N-PDSB; AAD12966. | | | |
| PT | New isolated dual-specificity phosphatase polypeptide for treating | | | |
| PT | cancer, graft-versus-host disease, autoimmune diseases, allergies, | | | |
| PT | metabolic diseases, abnormal cell growth and abnormal cell | | | |
| PT | proliferation - | | | |
| P3 | Claim 50; Fig 4; 81pp; English. | | | |
| CC | The present sequence is human dual-specificity phosphatase (DSP)-13 | | | |
| CC | protein. Inactivation of mitogen-activated protein kinase (MAP-kinase) | | | |
| CC | is mediated by dephosphorylation at a dual phosphorylation motif by DSP | | | |
| CC | which is referred to as MAP-kinase phosphatase. An agent that modulates | | | |
| CC | DSP is useful for treating a disorder selected from Duchenne muscular | | | |
| CC | dystrophy, cancer, graft-versus-host disease (GMD), autoimmune diseases, | | | |
| CC | allergies, metabolic diseases, abnormal cell growth, abnormal cell | | | |
| CC | proliferation and cell cycle abnormalities. DSP is useful for | | | |
| CC | identifying antibodies and other agents that inhibit DSP-12 and/or | | | |
| CC | DSP-13 activity. DSP and the agents identified are useful for | | | |
| CC | modulating cell proliferation, differentiation and survival. DSP is | | | |
| CC | useful in screening assays for modulators of enzyme activity and | | | |
| CC | substrate binding and for dephosphorylating a substrate of DSP-12 or | | | |
| CC | DSP-13. | | | |

| Seq | Sequence | 509 AA: |
|-----------------------|--|---|
| Query | March | 31.0%; Score 1058; DB 22; Length 509; |
| Best Local Similarity | 42.5%; | Pred. No. 3,4e-81; |
| Matches | 213; Conservative | 100; Pident. 134; Indels 54; Gaps 7 |
| QY | QSPFAVLRAVAVGLDGDGNDDAAEASSEPTKAPSEEEIHGDQDTFGQSGSGSPQOEQ | 94 |
| DB | ESFLTKVKAALFLPR----- | 74 |
| QY | 95 -----RQHLMVOLLPRDODIRLAOLEAPRPRLRYLVYSTRREGSLQSDETVLIG | 148 |
| DB | 75 KHAGDLOOHLAMFLLRPEDNIRLAVRLSEYYQNRTRVMVVSINGRO--DTEESIVLG | 132 |
| QY | 149 VDFPSSSPSCITGLGVLPMSPTQVYLVLDGSGFVTSGGOSRIKPIRISQIYMWATLVQVH | 208 |
| DB | 133 MDFSNDSTCTMGVLVPLMSDTLHLDDGSGFVSTQNRVHIFKPVSVQAMWALQSH | 192 |
| QY | 209 QACEAALGSLVPGGSALTWASHYQERLNSQSCINQEWATYADLESRLP--PSAEPGSS | 266 |
| DB | 193 KACEVAFRAHNYPGSLFLTWVSYYESHINSDQSVNEMWAMQDVQSHRPSALFTDIPT | 252 |
| QY | 267 EOEQGEQAIRLEIMKVLVDVSDIEVTSKRIQALRLGLPLQOYRDFDQMLLVQR | 326 |
| DB | 253 ERERERLIKTYLRITIMOKDENTISKEIRLELMQMCNIREREFIDNMTYILGM | 312 |
| QY | 327 DPASRIPEHLVIGSEWNAANTEELQNRVTHILNVAAREIDNYPFRFTYHNVRLWDEBSA | 386 |
| DB | 313 DSPQIFEFHVFLGSEWNASNIEDLNQRGVRYILNTVREIDNFPFGVEYHNRVYDEEAT | 372 |
| QY | 387 QLPFWKETHRTIEAARAQGTIVLVCKKGVGSRSAATYLAVMKQYEGLEALAHVQL | 446 |
| DB | 373 DLLAWMNDTYKFTISAKKHGSKCLVCKKGVSRASATYLAVMKRYGMWLDRAVDYKER | 432 |
| QY | 447 RPIARPNGFLRQLOIYOGILTVASRQSHWEQXGVSPDEHPAPEVSTPFP-----PLP | 501 |
| DB | 433 RTVTKPNSFPMQLEHYGIIILASTGLIH-----GG---RDKPWEKSKTFEFSVLVSTP | 485 |
| QY | 502 PEPEGGEEKVGVMEESQAP | 522 |
| DB | 486 GSPSCNPEKLIHISHPYLTP | 506 |
| RESULT 14 | | |
| AAE07044 | | |
| ID | AAE07044 | standard; Protein; 509 AA. |
| XX | AAE07044; | |
| AC | AAE07044; | |
| XX | 16-OCT-2001 | (first entry) |
| DT | 16-OCT-2001 | (first entry) |
| DE | Human dual-specificity phosphatase (DSP)-13 mutant protein, D360A. | |
| XX | Human; dual-specificity phosphatase; DSP-13; dual phosphorylation motif; | |
| RV | mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease; | |
| KW | GvHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; | |
| KM | allergy; metabolic disease; cell growth; cell proliferation; cytosolic; | |
| KM | cell cycle abnormality; cell differentiation; anti-leukemic; muscular; | |
| XX | Immunosuppressive; mutant; mutagen; variant. | |
| XX | Homo sapiens. | |
| OS | Synthetic. | |
| XX | Key | Location/Qualifiers |
| FT | Misc-difference 368 | /note= "Wild type Asp substituted with Ala" |
| XX | W0200157221-A2. | |
| XX | 09-AUG-2001. | |
| XX | 01-FEB-2001; 2001WO-US03429. | |

| | |
|----|---|
| XX | 02-FEB-2000; 200CUTS-0179886. |
| XX | (CEPT) - CEPYR INC. |
| XX | Luche RM, Wei B; |
| DR | WPJ; 2001-468887/53. |
| XX | |
| PS | New isolated dual-specificity phosphatase polypeptide for treating |
| PT | cancer, graft-versus-host disease, autoimmune diseases, allergies, |
| PT | metabolic diseases, abnormal cell growth and abnormal cell |
| PT | proliferation - |
| XX | |
| PS | Disclosure; Page -: 81pp; English. |
| XX | |
| CC | The present sequence is human dual-specificity phosphatase (DSP)-13 |
| CC | mutant protein, D368A. Inactivation of mitogen-activated protein kinase |
| CC | (MAP-kinase) is mediated by dephosphorylation at a dual phosphorylation |
| CC | motif by DSP which is referred to as MAP-kinase phosphatase. An agent |
| CC | that modulates DSP is useful for treating a disorder selected from |
| CC | Duchenne muscular dystrophy, cancer, graft-versus-host disease (GVHD), |
| CC | autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, |
| CC | abnormal cell proliferation and cell cycle abnormalities. DSP is useful |
| CC | for identifying antipodics and other agents that inhibit DSP-12 and/or |
| CC | DSP-13 activity. DSP and the agents identified are useful for |
| CC | modulating cell proliferation, differentiation and survival. DSP is |
| CC | useful in screening assays for modulators of enzyme activity and |
| CC | substrate binding and for dephosphorylating a substrate of DSP-12 or |
| CC | DSP-13. |
| CC | Note: The present sequence is not shown in the specification, but is |
| CC | derived from the DSP-13 sequence (AA06775) given as SEQ ID NO: 6 in |
| CC | figure 4. |
| SQ | Sequence 509 AA: |
| XX | |
| XX | Query Match 30.8%; Score 1050; DB 22; Length 509; |
| XX | Best Local Similarity 42.3%; Pred. No. 1,66-80; |
| XX | Matches 212; Conservative 100; Mismatches 15; Indels 54; Gaps 7 |
| OY | 36 QSFPAVLGAAYGLDGGDNDAEASSTPEKASEELHGDQTFGQSQSPOKEEQ-94 |
| DB | EELFRTYKAALFLPR-----GNGSTPRLSHRN 74 |
| OY | 95 -----RCCHLMVQLLRPRODIRLAQALEAPREPRRLYLVSITREGELSODETVLIG 148 |
| DB | 75 KHAAGDLQQHLQAMFILRPEDNIRLAVALSESTYQNRRIRNVVSTNGRQ--DTRESIVLG 132 |
| OY | 149 VDFPDSSSPECTGLVLPWSDPYVDLDGDSFGFSVGSGSRIFKPISIQTMATLVIA 208 |
| DB | 133 MDPSNDSSCTMGGLVPLMSDTTLIHDGGSFVSIDNRVAIFKPVSVQAMMSALQSLH 192 |
| OY | 209 QAEEALGGGLVPGSGALTMAHYERLNSSQCLNEMTMADELSLRP--PEAREGGS 266 |
| DB | 193 KAEEVARAHNYPGSLFTWSYSYSHINSQSSVENNAQDVQSHRPPSPALFTDIP 252 |
| OY | 267 EGEOMCAIRAEIMKVLDVDESSTSKETIQALEELRGLPLQOYRFINOMILLVAQR 326 |
| DB | 253 ERRTERRLLIKTLREIMQKDELNTSKETIELEMVCNLRFKKFDINEMIVILQM 312 |
| OY | 327 DRASRIFFPLYLYGSEMANALEELORNAVTHILMAREINDFYERTTYNVKLMDESA 386 |
| DB | 313 DSPTQIFHEVFPLGSEMNANLNLEDLCNRGRVILNWTRIEDNFEGVEYNINIVYAEN 372 |
| OY | 387 QLDPHKETHRFRLEBAROGGTIVLVHCWGYSRSAAATVLAAMYQYCSLEOLRHVOEL 446 |
| DB | 373 DLLAVMYNDYTKISRAKKHGSKCLVHCMSGYSRSBSASTVIAYAMEYGMNDRAVDYKER 432 |
| OY | 447 RPIARBNPFRLQLOLIYOGILITASKQHWMEQKGVGPSPEHPAPEVSTFP-----PLP 501 |
| DB | 433 RTVTKENPSEFMQLTEYOGILLASFGLIH---GG---RDKPKGEKSTFEESVDLWSIP 485 |
| OY | 502 PEEGGGGERKVMGESQAP 522 |

DB 486 GSPSCNPEKXLIHSHPLYLP 506

RESULT 15
AAE07045
ID AAE07045 standard; Protein; 509 AA.
XX
XX AAE07045;
XX
XX 16-OCT-2001 (first entry)
XX
XX Human dual-specificity phosphatase (DSP)-13 mutant protein, C399S.
XX
XX Human; dual-specificity phosphatase; DSP-13; dual phosphorylation motif; mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease; GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; allergy; metabolic disease; cell growth; cell proliferation; cytostatic; cell cycle abnormality; cell differentiation; antiallergic; muscular; immunosuppressive; mutant; mutein; variant.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 399 /note="Wild type Cys substituted with Ser"
XX
XX WO200157221-A2.
XX
XX 09-AUG-2001.
XX
XX 01-FEB-2001; 2001WO-US03429.
XX
XX 02-FEB-2000; 2000US-0179886.
XX
XX (CEPT-) CEPTVR INC.
XX
XX Lucche RM, Wei B;
XX
XX WPI; 2001-488887/53.
XX
XX
XX New isolated dual-specificity phosphatase polypeptide for treating cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation -
XX
XX Disclosure; Page -: 81pp; English.
XX
XX The present sequence is human dual-specificity phosphatase (DSP)-13 mutant protein, C399S. Inactivation of mitogen-activated protein kinase (MAP-kinase) is mediated by dephosphorylation at a dual phosphorylation motif by DSP which is referred to as MAP-kinase phosphatase. An agent that modulates DSP is useful for treating a disorder selected from Duchenne muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and other agents that inhibit DSP-12 and/or DSP-13 activity. DSP and the agents identified are useful for modulating cell proliferation, differentiation and survival. DSP is useful in screening assays for modulators of enzyme activity and substrate binding and for dephosphorylating a substrate of DSP-12 or DSP-13.
XX
XX Note: The present sequence is not shown in the specification, but is derived from the DSP-13 sequence (AAE06775) given as SEQ ID NO: 6 in figure 4.
XX
XX
XX Sequence 509 AA;
SQ

Query Match 30.7%; Score 1048; DB 22; Length 509;
Best Local Similarity 42.3%; Pred. No. 2.4e-80;
Matches 212; Conservative 100; Mismatches 135; Indels 54; Gaps 7;

QY 36 QSFALVGAIVIGLDGGNDDAEASSEPTKAPSEELHGDQTDPGGSGSQSFQKQBEQ- 94

DB 46 ESFLTVKGAALFLPR-----GNGSSTPRISHRN 74
QY 95 -----RQHLMVOLLARPODDIRLAQLARPRPRRLVLLVSTRBEGSLSOEETVLG 148
DB 75 KIAQDLQOHLQAMFLPLRPEDNIRLAVRLBSTYQNRIRVAVSTNGRQ--DTRESITVLG 132
QY 149 VDFPDSSSPSCCTLGLVLPMSDVOYVLDGDDGFSVYSGGSRIFKPIISIQTMATLQYLA 208
DB 133 MDFSNDSTCTMGVLVPLMSDTLILHDGDSGFSVTNRVHIFKPVSVQAMGALQSLH 192
QY 209 QACEAALSGLVPGGSALTMAHYOERLNSQSCLENTAMADLESIRP--PSAEPGSS 266
DB 193 KACEVAPARAHNYPGSLFLTWVSYESHINSQSSVNEWNAQDVQSHRDPSPALFTDIPT 252
QY 267 EOEOMEQAIRAELMWLVNDSVTSKEIRQALERLGLPQQYRDFIDNQMLLVAQR 326
DB 253 EHERTERLIKTKRIMNQKDLNTEKIRTELEMQVVCNLRFEKRIDEMIVILGQM 312
QY 327 DRASRIFFHLVYGSSEWNAANLELQNRNVTILNAREIDNPFYERFYNVRLMDESA 386
DB 313 DSPTQIFEHVFLGSEWNASNLEDLQNRGVRYILNVTREIDNPFQVFEYHNIRVYDEBAT 372
QY 387 QLEPHMKETHRPTEAARAQGTHTLVHCKMGVSRSAATVLAAMKQVECSLEQALRHQEL 446
DB 373 DLAYMNDIYKTIKAKKHGSKCLVHSMGYSRSASTIYAYAMKEYGNNDRAVDYKER 432
QY 447 RPIARPNGFRLQLOIYQGIILTASRQSHWEQKVGVSPEEHPAPEVSTPP-----PLP 501
DB 433 RTVTKPNSFMRQLREYQGIILASFLGIH-----GG---RDKPMGEKSTESVLDVLSIP 485
QY 502 PEPGEGEKKVGMESQAP 522
DB 486 GSPSCNPEKXLIHSHPLYLP 506

Search completed: January 15, 2004, 06:48:27
Job time : 76 secs

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CM protein - protein search, using sw model

Run on: January 15, 2004, 06:49:26 (Search time 39 Seconds)

(Without alignments)
3455.208 Million cell updates/sec

Title: US-09-955-732-2

Perfect score: 3412

Sequence: 1 MALVTVSRSPPGSGASTPVG.....RFRKVVQASVHDSGEEGA 659

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 3412 | 100.0 | 659 | 10 | US-09-955-732-2 |
| 2 | 3402 | 99.7 | 659 | 10 | US-09-955-732-2 |
| 3 | 2863 | 83.9 | 779 | 12 | US-10-363-676-11 |
| 4 | 2623 | 76.9 | 513 | 12 | US-10-108-260A-7517 |
| 5 | 2426 | 71.1 | 471 | 10 | US-09-761-640-4 |
| 6 | 2426 | 71.1 | 471 | 10 | US-09-955-732-21 |
| 7 | 2051.5 | 60.1 | 408 | 10 | US-09-761-640-6 |
| 8 | 1470.5 | 43.1 | 312 | 10 | US-09-761-640-8 |
| 9 | 1136 | 33.3 | 703 | 12 | US-10-108-260A-3142 |
| 10 | 1058 | 31.0 | 509 | 9 | US-09-775-925-6 |
| 11 | 1058 | 31.0 | 509 | 10 | US-09-955-732-14 |
| 12 | 1005 | 29.5 | 484 | 12 | US-10-181-590-9 |
| 13 | 971 | 28.5 | 552 | 9 | US-09-775-925-2 |
| 14 | 971 | 28.5 | 552 | 10 | US-09-955-732-15 |
| 15 | 918.5 | 26.9 | 524 | 10 | US-09-761-640-9 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|----|-------------------|-------------------|
| 15 | 914.5 | 26.8 | 737 | 10 | US-09-955-732-13 | Sequence 13, Appl |
| 17 | 911 | 26.7 | 986 | 12 | US-10-381-333-7 | Sequence 7, Appl |
| 18 | 581.5 | 17.0 | 140 | 10 | US-09-955-732-12 | Sequence 12, Appl |
| 19 | 581.5 | 17.0 | 141 | 12 | US-10-363-676-2 | Sequence 2, Appl |
| 20 | 578 | 16.9 | 111 | 10 | US-09-761-640-10 | Sequence 10, Appl |
| 21 | 574 | 16.8 | 241 | 9 | US-09-775-925-8 | Sequence 8, Appl |
| 22 | 539 | 15.8 | 244 | 12 | US-10-240-145-81 | Sequence 81, Appl |
| 23 | 539 | 15.8 | 244 | 15 | US-10-239-131-29 | Sequence 29, Appl |
| 24 | 521 | 15.3 | 170 | 9 | US-09-775-925-31 | Sequence 31, Appl |
| 25 | 512 | 15.0 | 170 | 9 | US-09-775-925-32 | Sequence 32, Appl |
| 26 | 497 | 14.6 | 458 | 15 | US-10-103-313-362 | Sequence 362, App |
| 27 | 323 | 9.5 | 109 | 12 | US-10-363-676-6 | Sequence 6, Appl |
| 28 | 280 | 8.2 | 139 | 12 | US-10-052-648A-83 | Sequence 83, Appl |
| 29 | 278 | 8.1 | 139 | 12 | US-10-052-648A-84 | Sequence 84, Appl |
| 30 | 254 | 7.4 | 217 | 9 | US-09-815-419-2 | Sequence 81, Appl |
| 31 | 254 | 7.4 | 217 | 12 | US-10-405-808-2 | Sequence 2, Appl |
| 32 | 253.5 | 7.4 | 665 | 9 | US-09-816-494-2 | Sequence 2, Appl |
| 33 | 253.5 | 7.4 | 665 | 10 | US-09-964-277-2 | Sequence 2, Appl |
| 34 | 252 | 7.4 | 171 | 12 | US-10-405-808-21 | Sequence 21, Appl |
| 35 | 247.5 | 7.3 | 665 | 12 | US-10-094-899-47 | Sequence 2312, Ap |
| 36 | 239.5 | 7.0 | 444 | 10 | US-09-964-899-47 | Sequence 47, Appl |
| 37 | 239.5 | 7.0 | 482 | 12 | US-10-346-356-2 | Sequence 2, Appl |
| 38 | 237.5 | 7.0 | 172 | 9 | US-09-816-494-8 | Sequence 8, Appl |
| 39 | 237.5 | 7.0 | 172 | 9 | US-09-815-419-5 | Sequence 5, Appl |
| 40 | 237.5 | 7.0 | 172 | 12 | US-10-165-272-5 | Sequence 5, Appl |
| 41 | 237.5 | 7.0 | 172 | 12 | US-10-410-764-133 | Sequence 133, App |
| 42 | 234 | 6.9 | 173 | 9 | US-09-815-494-7 | Sequence 7, Appl |
| 43 | 234 | 6.9 | 173 | 9 | US-09-815-419-4 | Sequence 4, Appl |
| 44 | 234 | 6.9 | 173 | 12 | US-10-165-272-4 | Sequence 4, Appl |
| 45 | 234 | 6.9 | 173 | 12 | US-10-363-676-5 | Sequence 5, Appl |

RESULT 1
US-09-955-732-2
Application US/09955732
Publication No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955.732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 659
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-732-2

Query Match 100.0%; Score 3412; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 4, 2e-263;
Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 SCINWTAMADLESLRPPSABPSSGSSSEOEOMEQALRAELMKVLDVSDLESVTSKEIRQAL 300
 DB 241 SCINWTAMADLESLRPPSABPSSGSSSEOEOMEQALRAELMKVLDVSDLESVTSKEIRQAL 300
 QY 301 EURLGLPQQYRDIDNOMLLVAQRDASRIFFPHLYGSEMANAANTEELORNVTHILN 360
 DB 301 EURLGLPQQYRDIDNOMLLVAQRDASRIFFPHLYGSEMANAANTEELORNVTHILN 360
 QY 361 MAREIDNFFPERFTYHNVRIMDEBSAQLPHMKETHRFTEAARAOQTHVLVHCKMGVSRS 420
 DB 361 MAREIDNFFPERFTYHNVRIMDEBSAQLPHMKETHRFTEAARAOQTHVLVHCKMGVSRS 420
 QY 421 AATVLAAMKQYECESLQALRHVOELRPIARPNGFLRQLOIQGILITASROSHWEGKY 480
 DB 421 AATVLAAMKQYECESLQALRHVOELRPIARPNGFLRQLOIQGILITASROSHWEGKY 480
 QY 481 GGVSPEEHAPAEVSTPPPLPPEEGGEEKYVGMESQAAPKEBGPFRINLRGVMS 540
 DB 481 GGVSPEEHAPAEVSTPPPLPPEEGGEEKYVGMESQAAPKEBGPFRINLRGVMS 540
 QY 541 ISLPESELESTSETSDMEVEVSSHSSHEEPLOFPOLARTKGQGVDRGPALKSR 600
 DB 541 ISLPESELESTSETSDMEVEVSSHSSHEEPLOFPOLARTKGQGVDRGPALKSR 600
 QY 601 QSVYTLQGSAAVANRTOAFQOEQGGQGGGECPCISTPRFRKVVYQASVHDSGEGEA 659
 DB 601 QSVYTLQGSAAVANRTOAFQOEQGGQGGGECPCISTPRFRKVVYQASVHDSGEGEA 659

RESULT 2

US-09-761-640-5
 ; Sequence 5, Application US/09761640
 ; Patent No. US20020137042A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
 ; FILE REFERENCE: CLO00964-CIP
 ; CURRENT APPLICATION NUMBER: US/09/761,640
 ; NUMBER FILING DATE: 2001-01-18
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 659
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-761-640-5

Query Match 99.7%; Score 3402; DB 10; Length 659;
 Best Local Similarity 99.8%; Pred. No. 2,66-262;
 Matches 659; Conservative 1; Indels 0; Gaps 0;

QY 1 MALVTVSRSPGSGASTPVGPMDQAVORRSRLORROSFAVLRGAVLGLQDGGDNDAAEA 60
 DB 1 MALVTVSRSPGSGASTPVGPMDQAVORRSRLORROSFAVLRGAVLGLQDGGDNDAAEA 60
 QY 61 SEPEPKASEEELIGDCTDPGQSGSQKOEORQHLMVOLLRQDDIRLAQLEAP 120
 DB 61 SEPEPKASEEELIGDCTDPGQSGSQKOEORQHLMVOLLRQDDIRLAQLEAP 120
 QY 121 RPRRLRYLLVSTRREGSLQDETVLLGVDPFDSSEPCITGLVPLMSDVOYLLDDGG 180
 DB 121 RPRRLRYLLVSTRREGSLQDETVLLGVDPFDSSEPCITGLVPLMSDVOYLLDDGG 180
 QY 181 FSVTSGGQGRIFKPISTQMTATLOVLMQACEALGSLVGGGALTMASHYQERLNSQ 240
 DB 181 FSVTSGGQGRIFKPISTQMTATLOVLMQACEALGSLVGGGALTMASHYQERLNSQ 240
 QY 241 SCINWTAMADLESLRPPSABPSSGSSSEOEOMEQALRAELMKVLDVSDLESVTSKEIRQAL 300
 DB 241 SCINWTAMADLESLRPPSABPSSGSSSEOEOMEQALRAELMKVLDVSDLESVTSKEIRQAL 300

QY 301 EURLGLPQQYRDIDNOMLLVAQRDASRIFFPHLYGSEMANAANTEELORNVTHILN 360
 DB 301 EURLGLPQQYRDIDNOMLLVAQRDASRIFFPHLYGSEMANAANTEELORNVTHILN 360
 QY 361 MAREIDNFFPERFTYHNVRIMDEBSAQLPHMKETHRFTEAARAOQTHVLVHCKMGVSRS 420
 DB 361 MAREIDNFFPERFTYHNVRIMDEBSAQLPHMKETHRFTEAARAOQTHVLVHCKMGVSRS 420
 QY 421 AATVLAAMKQYECESLQALRHVOELRPIARPNGFLRQLOIQGILITASROSHWEGKY 480
 DB 421 AATVLAAMKQYECESLQALRHVOELRPIARPNGFLRQLOIQGILITASROSHWEGKY 480
 QY 481 GGVSPEEHAPAEVSTPPPLPPEEGGEEKYVGMESQAAPKEBGPFRINLRGVMS 540
 DB 481 GGVSPEEHAPAEVSTPPPLPPEEGGEEKYVGMESQAAPKEBGPFRINLRGVMS 540
 QY 541 ISLPESELESTSETSDMEVEVSSHSSHEEPLOFPOLARTKGQGVDRGPALKSR 600
 DB 541 ISLPESELESTSETSDMEVEVSSHSSHEEPLOFPOLARTKGQGVDRGPALKSR 600
 QY 601 QSVYTLQGSAAVANRTOAFQOEQGGQGGGECPCISTPRFRKVVYQASVHDSGEGEA 659
 DB 601 QSVYTLQGSAAVANRTOAFQOEQGGQGGGECPCISTPRFRKVVYQASVHDSGEGEA 659

RESULT 3

US-10-363-676-11
 ; Sequence 11, Application US/10363676
 ; Publication No. US20030170856A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer AG
 ; TITLE OF INVENTION: REGULATION OF HUMAN MAP KINASE PHOSPHATASE-LIKE ENZYME
 ; FILE REFERENCE: LIO122 Foreign Countries
 ; CURRENT APPLICATION NUMBER: US/10/363,676
 ; CURRENT FILING DATE: 2003-03-06
 ; PRIOR APPLICATION NUMBER: US 60/230,709
 ; PRIOR FILING DATE: 2000-09-07
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 779
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: NAME/KEY: MISC FEATURE
 ; LOCATION: (701)..(701)
 ; OTHER INFORMATION: Xaa-any amino acid
 ; US-10-363-676-11

Query Match 83.9%; Score 2863; DB 12; Length 779;
 Best Local Similarity 84.6%; Pred. No. 36-219;
 Matches 581; Conservative 19; Mismatches 39; Indels 48; Gaps 11;

QY 9 SPSSGASTPVGP-----WDQAVORRSRLORROSFAVLRL--- 42
 DB 24 APVAAGASTALMGGIPEREGTALPALTALGSLRQDDLVORRSRLQRR---ALRSC 79
 QY 43 GAVIGLDGGDNDAAASSEPTTEKAPSEELH-GDOTFG-QGSGPOKOEORQHLM 100
 DB 80 GAVIGLDGGDNDAAASSEPTTEKAPSEELHGGTQTFRCQDPVPSRRSGNCL 139
 QY 101 MVOLLRQDDIRLAQLEA-----PPEPLRYLLVSTRREGSLQDETVL---LGYD 150
 DB 140 MV---RRAAAGMTSDLEAQAQGTGPGIRIPCLVAVSTRREG---RSEPRRRSWDVD 193
 QY 151 PPDSSSPCTGLVPLMSDVOYLLDGGGFSVTSGGQGRIFKPISTQMTATLOVLMQ 210
 DB 194 PPDSSSPCTGLVPLMSDVOYLLDGGGFSVTSGGQGRIFKPISTQMTATLOVLMQ 253
 QY 211 CEALGSLVPGGSLTMASHYQERLNSQSCINWTAMADLESLRPPSABPSSGSSSEOE 270
 DB 254 CEALGSLVPGGSLTMASHYQERLNSQSCINWTAMADLESLRPPSABPSSGSSSEOE 313

QY 271 MEQAIRAEIMKVLVDVSDLESVTSKEIRQALELRLGLPLQOYRDFIDNQMLLVAAQRDPA 330
 DB 314 MERAIRAEIMKVLVDVSDLESVTSKEIRQALELRLGLPLQOYRDFIDNQMLLVAAQRDPA 373
 QY 331 RIFPHVLGSEBMANLBELOKRVTHILMARINDFYPERFTYHNVRLMDESSQILP 390
 DB 374 RIFPHVLGSEBMANLBELOKRVTHILMARINDFYPERFTYHNVRLMDESSQILP 433
 QY 391 HMKETHRIFEAARQGTHTLVHCKMGVSRSAATVLAAMKQYCSLEQALRHVOELRPIA 450
 DB 434 HMKETHRIFEAARQGTHTLVHCKMGVSRSAATVLAAMKQYCSLEQALRHVOELRPIA 493
 QY 451 RPNNGFLRQLOIYQGITLTSRQSHVWPKYCGVSRPHEHPAPEVSTPPPLPPEPEGGE 510
 DB 494 RPNNGFLRQLOIYQGITLTSRQSHVWPKYCGVSRPHEHPAPEVSTPPPLPPEPEGGE 553
 QY 511 KVVMEESQAAPKEEPGRPRINLRGVMSISLLEPSLEESTSETSDMPEVSSHSSH 570
 DB 554 KVVMEESQAAPKEEPGRPRINLRGVMSISLLEPSLEESTSETSDMPEVSSHSSH 613
 QY 571 EEPLOPPOLARTKGQOVDRGPOPALKSQSVTLTQGSVVANRTQAFQEOEQGQGO 630
 DB 614 EEPLOPPOLARTKGQOVDRGPOPALKSQSVTLTQGSVVANRTQAFQEOEQGQGO 673
 QY 631 GEPICISSTPRFRKVVROASVHDSGEEG 657
 DB 674 GEPICISSTPRFRKVVROASVHDSGEEG 700

RESULT 4

US-10-108-260A-2517
 ; Sequence 2517, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108, 260A
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2517
 ; LENGTH: 513
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-108-260A-2517

Query Match 76.9%; Score 2623; DB 12; Length 513;
 Best Local Similarity 99.0%; Pred. No. 2.2e-200;
 Matches 506; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 151 FP--DSSPSCGTLGLVPLMSDTPQVYLDGQGFVTSQGSRIFKPISIQTMATLQVHL 208
 DB 3 PPLSPASSPSCGTLGLVPLMSDTPQVYLDGQGFVTSQGSRIFKPISIQTMATLQVHL 62
 QY 209 QACEAALGSGLVPGSALTMASHYQERLNSBOCLINMTWADLESIRPSPAGGSSQ 268
 DB 63 QACEAALGSGLVPGSALTMASHYQERLNSBOCLINMTWADLESIRPSPAGGSSQ 122
 QY 269 EQMOCARAEIMKVLVDVSDLESVTSKEIRQALELRLGLPLQOYRDFIDNQMLLVAAQRD 328
 DB 123 EQMOCARAEIMKVLVDVSDLESVTSKEIRQALELRLGLPLQOYRDFIDNQMLLVAAQRD 182
 QY 329 ASRIFPHVLGSEBMANLBELOKRVTHILMARINDFYPERFTYHNVRLMDESSQIL 388
 DB 183 ASRIFPHVLGSEBMANLBELOKRVTHILMARINDFYPERFTYHNVRLMDESSQIL 242
 QY 389 LPHKETHRIFEAARQGTHTLVHCKMGVSRSAATVLAAMKQYCSLEQALRHVOELR 448
 DB 243 LPHKETHRIFEAARQGTHTLVHCKMGVSRSAATVLAAMKQYCSLEQALRHVOELR 302
 QY 449 IARNPGLRQLOIYQGITLTSRQSHVWPKYCGVSRPHEHPAPEVSTPPPLPPEPEGGE 508

DB 303 IARNPGLRQLOIYQGITLTSRQSHVWPKYCGVSRPHEHPAPEVSTPPPLPPEPEGGE 362
 QY 509 EKVVMESQAAPKEEPGRPRINLRGVMSISLLEPSLEESTSETSDMPEVSSHSS 568
 DB 363 GKVVMESQAAPKEEPGRPRINLRGVMSISLLEPSLEESTSETSDMPEVSSHSS 422
 QY 569 SHEEPLOPPOLARTKGQOVDRGPOPALKSQSVTLTQGSVVANRTQAFQEOEQGQGO 628
 DB 423 SHEEPLOPPOLARTKGQOVDRGPOPALKSQSVTLTQGSVVANRTQAFQEOEQGQGO 482
 QY 629 GQGEPCISSTPRFRKVVROASVHDSGEEGA 659
 DB 483 GQGEPCISSTPRFRKVVROASVHDSGEEGA 513

RESULT 5

US-09-761-640-4
 ; Sequence 4, Application US/09761640
 ; Patent No. US20020137042A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al
 ; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
 ; FILE REFERENCE: CL000964-CIP
 ; CURRENT APPLICATION NUMBER: US/09/761, 640
 ; CURRENT FILING DATE: 2001-01-18
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 471
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-761-640-4

Query Match 71.1%; Score 2426; DB 10; Length 471;
 Best Local Similarity 100.0%; Pred. No. 9.8e-185;
 Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALTVSRSPSGASTPVPMDQAVORRSRQROSFAYLRGAVLGLQDGGDNDAAEA 60
 DB 1 MALTVSRSPSGASTPVPMDQAVORRSRQROSFAYLRGAVLGLQDGGDNDAAEA 60
 QY 61 SSEPTEKAPSEBELHGDQTFQGGSQSPQKEBQRHLLHWOLRPQDDIRLAQLEAP 120
 DB 61 SSEPTEKAPSEBELHGDQTFQGGSQSPQKEBQRHLLHWOLRPQDDIRLAQLEAP 120
 QY 121 RPPRLRYLLVSTRREGGGLSODETVLLGVDFPDSSPSCGTLGLVPLMSDTPQVYLDGQGG 180
 DB 121 RPPRLRYLLVSTRREGGGLSODETVLLGVDFPDSSPSCGTLGLVPLMSDTPQVYLDGQGG 180
 QY 181 FSVTSGGQSRIFKPIISIQTMATLQVHLQACEAALGSGLVPGSALTMASHYQERLNSBO 240
 DB 181 FSVTSGGQSRIFKPIISIQTMATLQVHLQACEAALGSGLVPGSALTMASHYQERLNSBO 240
 QY 241 SCINMTWADLESIRPSPAGGSSBOEQOAIRAEIMKVLVDVSDLESVTSKEIRQAL 300
 DB 241 SCINMTWADLESIRPSPAGGSSBOEQOAIRAEIMKVLVDVSDLESVTSKEIRQAL 300
 QY 301 ELRLGLPLQOYRDFIDNQMLLVAAQRDASRIFFPHVLGSEBMANLBELOKRVTHILN 360
 DB 301 ELRLGLPLQOYRDFIDNQMLLVAAQRDASRIFFPHVLGSEBMANLBELOKRVTHILN 360
 QY 361 MARSDINFPYPERFTYHNVRLMDESSQILPHKETHRIFEAARQGTHTLVHCKMGVSR 420
 DB 361 MARSDINFPYPERFTYHNVRLMDESSQILPHKETHRIFEAARQGTHTLVHCKMGVSR 420
 QY 421 AATVLAAMKQYCSLEQALRHVOELRPIARNPGLRQLOIYQGITLTA 469
 DB 421 AATVLAAMKQYCSLEQALRHVOELRPIARNPGLRQLOIYQGITLTA 469

```

RESULT 6
US-09-955-732-21
; Sequence 21, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.453
; CURRENT APPLICATION NUMBER: US/09/955.732
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-955-732-21

Query Match      71.1%; Score 2426; DB 10; Length 471;
Best Local Similarity 100.0%; Pred. No. 9.8e-185;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
DB 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
QY 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
DB 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
QY 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180
DB 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180
QY 181 FSVTSGGSGSRIFPKISIQTMWATLQVHQAEEALGSLVPGSALTWASHYQERLNSQ 240
DB 181 FSVTSGGSGSRIFPKISIQTMWATLQVHQAEEALGSLVPGSALTWASHYQERLNSQ 240
QY 241 SCLENTMTADLESIRPPSAPPGSSSEQEQMEQAIRAEMLKVLVDSDLESVTSKEIRQAL 300
DB 241 SCLENTMTADLESIRPPSAPPGSSSEQEQMEQAIRAEMLKVLVDSDLESVTSKEIRQAL 300
QY 301 ELRLGLPQOYRDFIDNQMILLVAQRDPASRIFFHLVYGSWMANLLELQRNVTHILN 360
DB 301 ELRLGLPQOYRDFIDNQMILLVAQRDPASRIFFHLVYGSWMANLLELQRNVTHILN 360
QY 361 MAREIDNFPERFFYHNVRLEWDESAQLLPWKETHRIEAPARQGHVHVHCKMGYSRS 420
DB 361 MAREIDNFPERFFYHNVRLEWDESAQLLPWKETHRIEAPARQGHVHVHCKMGYSRS 420
QY 421 AATVLAAMKQYECGLEQALRHVQELRPIARPNGFLRQLQIYQIGILTA 469
DB 421 AATVLAAMKQYECGLEQALRHVQELRPIARPNGFLRQLQIYQIGILTA 469

RESULT 7
US-09-761-640-6
; Sequence 6, Application US/09761640
; Patent No. US20020137042A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00964-CIP
; CURRENT APPLICATION NUMBER: US/09/761.640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 408
; TYPE: PRT

```

```

; ORGANISM: Human
US-09-761-640-6

Query Match      60.1%; Score 2051.5; DB 10; Length 408;
Best Local Similarity 86.6%; Pred. No. 5.6e-155;
Matches 406; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

QY 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
DB 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
QY 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
DB 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
QY 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180
DB 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180
QY 181 FSVTSGGSGSRIFPKISIQTMWATLQVHQAEEALGSLVPGSALTWASHYQERLNSQ 240
DB 181 FSVTSGGSGSRIFPKISIQTMWATLQVHQAEEALGSLVPGSALTWASHYQERLNSQ 240
QY 241 SCLENTMTADLESIRPPSAPPGSSSEQEQMEQAIRAEMLKVLVDSDLESVTSKEIRQAL 300
DB 241 SCLENTMTADLESIRPPSAPPGSSSEQEQMEQAIRAEMLKVLVDSDLESVTSKEIRQAL 300
QY 301 ELRLGLPQOYRDFIDNQMILLVAQRDPASRIFFHLVYGSWMANLLELQRNVTHILN 360
DB 301 ELRLGLPQOYRDFIDNQMILLVAQRDPASRIFFHLVYGSWMANLLELQRNVTHILN 360
QY 361 MAREIDNFPERFFYHNVRLEWDESAQLLPWKETHRIEAPARQGHVHVHCKMGYSRS 420
DB 361 MAREIDNFPERFFYHNVRLEWDESAQLLPWKETHRIEAPARQGHVHVHCKMGYSRS 420
QY 421 AATVLAAMKQYECGLEQALRHVQELRPIARPNGFLRQLQIYQIGILTA 469
DB 421 AATVLAAMKQYECGLEQALRHVQELRPIARPNGFLRQLQIYQIGILTA 469

RESULT 8
US-09-761-640-8
; Sequence 8, Application US/09761640
; Patent No. US20020137042A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00964-CIP
; CURRENT APPLICATION NUMBER: US/09/761.640
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Human
US-09-761-640-8

Query Match      43.1%; Score 1470.5; DB 10; Length 312;
Best Local Similarity 92.9%; Pred. No. 7.6e-109;
Matches 290; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
DB 1 MALVTSSPPGSGASTPVGPMDQAVQRSLQRQSFAYLRGAVLGLQDGGNDDAEA 60
QY 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
DB 61 SSEPTKAPSEBELHGDQTDPGQSGSPQKQEBQRCHLHMVQLRPQDDIRLAQLAP 120
QY 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180
DB 121 RPPRLRYLLVSTRREGSLQSDETVLLGVDPDSSSPSCTGLVPLMSDQVYLLDGG 180

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Db 121 RPPRLRLVLRVSTREGGLSODETVLGVFPDPSSSCTLGVLPLMSTQYVLDGDS 180
QY 181 FSVTSGGQSRIKFKPISIQTMWATLQVHQAEEALSGVLPGSALTWASHYQERLNSQ 240
Db 181 FSVTSGGQSRIKFKPISIQTMWATLQVHQAEEALSGVLPGSALTWASHYQERLNSQ 240
QY 241 SCINEMTAMADLESIRPEASBPSSGSGSCOMEQATRELMKVLDV--SDLESVTSKEIRQA 299
Db 241 SCINEMTAMADLESIRPEASBPSSGSGSCOMEQATRELMKVLELESTSETSMPEVFS 300
QY 300 LEIRLGLPLQY 311
Db 301 HESGHEERLOPF 312

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RESULT 9

```

US-10-108-260A-3142
; Sequence 3142, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108.260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3142
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3142

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```

Query Match 33.3%; Score 1136; DB 12; Length 703;
Best Local Similarity 42.9%; Pred. No. 1.1e-81;
Matches 256; Conservative 91; Mismatches 152; Indels 98; Gaps 17;

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QY 36 QSFAYLRGAVLGLDGGDNDDAEASSEPTKAPSEBEELHGDQTFGQGS-QSPQKOE-E 93
Db 51 ESFLVKGALFLPQ-----SSPQ-----GQSLQHPHKAGD 84
QY 94 QRHLHMVQLRPPDDIRLAQLEAPRPPRLRLVLRVSTREGGLSODETVLGVDP 151
Db 85 LPQHLOWMINLRCBEDRIKLAVRLESAMADRYRTMVVYSSGRQ---DTEENILLGVDF 140
QY 152 PDSSSPSCTLGVLPLMSTQYVLDGDSFVTSGGQSRIKFKPISIQTMWATLQVHQA 211
Db 141 SSKSKSCTIGWVLRIMSDTKIHLDGGGFSVSTAGRHIKFPVSVQAMMSALQVLRKAC 200
QY 212 EALGSGGLVPGSALTWASHYQERLNSQSCINEMTAMADLESIRP--PSAEPGSSSEOE 269
Db 201 EVARHNHYFPGVALIMATYTESCISSESCINEMTAMADLESIRPSPALFVDPKPEGE 260
QY 270 QMEQATRELMKVLDVSDLESVTSKEIRQALELGLPLQGYRDFINOMLLVAQRDA 329
Db 261 RTERLIKAKLRISIMMSQDLENVTSKEIRNELEKQNCMLKELFIDENMLLIGQMDKP 320
QY 330 SRIFPHLYLGEEMNANLELQNRVTHILNAREIDNFPYPERFTYHNRLMDESAQL 389
Db 321 SLIFPHLYLGEEMNANLELQNRVTHILNAREIDNFPYPERFTYHNRLMDESAQL 380
QY 330 PHMKETHRFFIETARQAGTHVLVCKMGVSRSAATYLAAMQYECSEQLARHQELRPI 449
Db 381 AHMNEYHFINKAKNHSKCLVHCXGVSRSASTVIAAMKEFMPLEKAYNVKQKRSI 440
QY 450 ARPNGFLRQLOIYQGITLARSQH--VMEQKVG--VSPREHDA-----PE 492
Db 441 TRPNNGFRQLSEYIGILDAKQKRNKLMRQCTSSLQGPVDDPAGPDPFLPDPDGPPE 500
QY 493 VSTP-----PLP-----PEPEGGEKRVYQME-----SQAP 522
Db 501 SQLPFLDDAAGPLGPPLPCCFRRLSDPLPSPEDETG--SLVHLEDPEREALLAEAP 557

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QY 523 KEE---PGPRPRLNRGVWRS-SLEPSL--ELESTSETSMPEVFSHESHEEPL 574
Db 558 PAEVTRPARQF-----QSGSLCEKDYKKLEBFGSKGSGSLQVLEETREEREG 607

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RESULT 10

```

US-09-775-925-6
; Sequence 6, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775.925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-6

```

```

Query Match 31.0%; Score 1058; DB 9; Length 509;
Best Local Similarity 42.5%; Pred. No. 1.2e-75;
Matches 213; Conservative 100; Mismatches 134; Indels 54; Gaps 7;

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QY 36 QSFAYLRGAVLGLDGGDNDDAEASSEPTKAPSEBEELHGDQTFGQGSQSPQKOEQ 94
Db 46 ESFLVKGALFLP-----SSPQ-----GQSLQHPHKAGD 84
QY 95 QRHLHMVQLRPPDDIRLAQLEAPRPPRLRLVLRVSTREGGLSODETVLGVDP 148
Db 75 KTAGDQLQHQLAMFILLRPEEDIRLAVRLESTYQKRTRYMVVSTNGRQ--DTESIVLG 132
QY 149 VDPSSSPSCTLGVLPLMSTQYVLDGDSFVTSGGQSRIKFKPISIQTMWATLQVH 208
Db 133 MDPSSNDSSCTGMLGVLPMSDILLHLDGGGFSVSTDRVHIFKPVSVQAMMSALQSLH 192
QY 209 QACEALSGGLVPGSALTWASHYQERLNSQSCINEMTAMADLESIRP--PSAEPGSS 266
Db 193 KACEVLRANHYFPGSLFLTWVSITESHNSDSSVEMNAMDVQSHRDSALFTDIT 252
QY 267 EOPMEQATRELMKVLDVSDLESVTSKEIRQALELGLPLQGYRDFINOMLLVAQR 326
Db 253 ERERTRLIKTLREIMQKDELNTSKEIRTELEWQVCNLRPEKXFIDNEMIVILQ 312
QY 327 DRASRIFPHLYLGEEMNANLELQNRVTHILNAREIDNFPYPERFTYHNRLMDESA 386
Db 313 DSEPTQFHFVPGSEMNANLELQNRVTHILNAREIDNFPYPERFTYHNRLMDESA 372
QY 387 QLPFWKETHRFFIETARQAGTHVLVCKMGVSRSAATYLAAMQYECSEQLARHQEL 446
Db 373 DLLAYNDYIKFKSKKKGKSCVLCXGVSRSASTVIAAMKEFGWMLDAVDYKSR 432
QY 447 RPIARNPGFLRQLOIYQGITLARSQSHVMEQKVGVSSEBHPAPVSTPFP-----PLP 501
Db 433 RVTYKPNPSFMQLEEYQGITLARSFLGLTH---GG---RDXFWGKSTEFESVDLVSTP 485
QY 502 PEPEGGEKRVYQME-----SQAP 522
Db 486 GSPSCCNPEKTLHISHPYLTP 506

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RESULT 11

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US-09-955-732-14
; Sequence 14, Application US/09955732
; Publication No. US20020182203A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.

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; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-955-732-14

Query Match
Best Local Similarity 42.5%; Score 1058; DB 10; Length 509;
Matches 213; Conservative 100; Mismatches 134; Indels 54; Gaps 7;

QY 36 OSFAVLGAVLGLQGGDNDAAEASSEPTKASEEELHGDQTFQGGSGSPQKQEQ-94
DB 46 ESFLVKGALFLPR-----GNGSSTPRISHRN 74
QY 95 -----RQHLHVLVOLARPODDIRLAQLEAPRPPRLRYLLVSTRREGGLSODETVLIG 148
DB 75 KHAGDLOQHLMAMFLLRPEDNIRLAVRLSESTYONKRRYVAVSTNGRQ--DTEESIVLG 132
QY 149 VDFPSSSPSCCTGLGLVPLMSDQYVLDGCGFSVTSGGGSRIFKPISTQTMATLQVHL 208
DB 133 MDFSNDSTCTMGVILPLMSDTHLHDGCGFSVSTDNKRVHIFKPIVQAMMSALQSLH 132
QY 209 QACEAALGSLVPGGSALTWASHYQERINSQSCLENWTAMADLESIRP--PSAEPGSS 266
DB 193 KACEVARAHANYPGSLFTLWVSYYESHINSQSSVNNMAMQDVQSHRPPSPALFTDIFT 252
QY 267 EOEQGEQAIRAEIWMVLDVSDLESVTSKEIRQALELRGLPQOYRDFINOMLLVAOR 326
DB 253 ERERERLIKTKLREIMQKDLNITSKEIRTELEMOMVCNLRPFKEFIDNEMVILGQM 312
QY 327 DRASRIFPHLYLGSEWNAANLEELQNRKVTHILMAREIDNIFYPERFTYNNVRLMDESA 386
DB 313 DSPQIFEHVFLGSEWNASNLEDLQNRGVRYLNVTRIEDNFFGVGEYHNIRVYDEAT 372
QY 387 QILPHMKETHRFIEAARQCTHVIVHCGMGVSRSAATVLYAMQYCSLEQALRHQEL 446
DB 373 DLLAWNDTYFKFISKAKGSKCLVHCQMGVSRASATVLYAMKEYGMNLDRAVDYKER 432
QY 447 RPIARPNGFLRQLOIYQGITLTAQRSHVMEQKGVSPREHPAPEVSTFEP-----PLP 501
DB 433 RTVTRKPNDSFMRQLEBYGILLASPIGLIH-----CG---RDKPWGEKSTPEVDIVSIP 485
QY 502 PEPEGGGEKXVGMEESSQAP 522
DB 486 GSPSCCNEXKLHISHPYLTP 506

RESULT 12
US-10-181-590-9
; Sequence 9, Application US/10181590
; Publication No. US20030152949A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: MATHUR, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAU, Preeti
; APPLICANT: WANG, Eureka
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: POLICKY, Jennifer L.
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: PI-0018 PCT

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; CURRENT APPLICATION NUMBER: US/10/181,590
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/177,719; 60/178,388; 60/184,959; 60/190,142
; PRIOR FILING DATE: 2000-01-21; 2000-01-28; 2000-02-25; 2000-03-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030152949A1 637331CD1
; US-10-181-590-9

Query Match
Best Local Similarity 40.7%; Score 1005; DB 12; Length 484;
Matches 211; Conservative 97; Mismatches 143; Indels 68; Gaps 8;

QY 1 MALTVSRSPGSGASTPVGPMDOAVQRRSRQRR---OSFAVLGAVLGLQGGDNDAA 57
DB 1 MALTVQRRSPFTSTSSPCASADSGEBECRQSPRSIESFLTVKQALFLPR-----53
QY 58 AASASEPTKEKASEEELHGDQTFQGGSGSPQKQEQ-----RQHLHVLVOLARPODD 110
DB 54 -----GNGSSTPRISHRNKHAGDLOQHLMAMFILLRPEDN 89
QY 111 IRLAQLEAPRPPRLRYLLVSTRREGGLSODETVLIGVDFPSSSPSCCTGLVPLMSD 170
DB 90 IRLAVRLSESTYONKRRYVAVSTNGRQ--DTEESIVLMDSSNSDSTCTMGVILPLMSD 147
QY 171 TQVYLDGCGFSVTSGGGSRIFKPISTQTMATLQVHLQACEAALGSLVPGGSALTWAS 230
DB 148 TLHHDGCGFSVSTDNKRVHIFKPIVQAMMSALQSLHFACEVARAHANYPGSLFTLWVS 207
QY 231 HYQERINSQSCLENWTAMADLESIRP--PSAEPGSSQEQMBAITAEILMKYLDVSD 288
DB 208 YESHINSQSSVNNMAMQDVQSHRPPSPALFTDIPERERTERLIKTKLREIMQKDL 267
QY 289 ESVTSKEIRQALELGLPQOYRDFINOMLLVAQRDRASRIFFPHLYLGSEWNAANLE 348
DB 268 ENITSKEIRTELEMOMVCNLRPFKEFIDNEMVILGQMDSPQIFEHVFLGSEWNASNLE 327
QY 349 ELQNRKVTHILMAREIDNIFYPERFTYNNVRLMDESAQILPHMKETHRFIEAARQCTH 408
DB 328 DLQNRGVRYLNVTRIEDNFFGVGEYHNIRYDEEATDLLAWNDTYFKFISKAKGSK 387
QY 409 VLVHCQMGVSRSAATVLYAMQYCSLEQA-----LHVQELRPIARPNGFLRQLOIY 463
DB 388 CLVHCQMGVSRASATVLYAMKEYGMNLDRASSRIKRYNNLSF-----DVCTF 438
QY 464 QGILTASRQSHVMEQKGVSPREHPAPEVSTFEPPLP 502
DB 439 PTMTI-----QIMNISITPKKFPYASISFSLSP 468

RESULT 13
US-09-775-925-2
; Sequence 2, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf W.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 552
; TYPE: PRT

```


ORGANISM: Homo sapiens
US-09-775-925-2

Query Match 28.5%; Score 971; DB 9; Length 552;
Best Local Similarity 44.6%; Pred. No. 1,1e-68;
Matches 208; Conservative 73; Mismatches 121; Indels 64; Gaps 11;

163 LVLPLMSDTQVYLLDGDGFSVTSQGSRIFFKPIISIQTMWATLQVLAQCEALGSGLVPG 222
1 MVLRLMSDTKHLDDGDFSVSTAGRMHIFKPVSVQAWMSALQVLAHKAACEVARRHNYPG 60
223 GSALTWASHYQERLNSQSCINEMTAMADLESRLP--PSAEPGSSSQEQMEQAIRAEIM 280
61 GVALIMATVYSCISSEQSCINEMWAMQDLESTRPDSPLFVDKPTGEERTERLIKAKLR 120
281 KVLVSPDLESTYSKEIRQALELRGLPLQOYRDFIDNOMLLVLAQRASRIFFPLYLGS 340
121 SIMSODLENTYSKEIRNELEKQNNCNLKEKEFIDNEMLLIQMKPSLIFDLVLGS 180
341 EMNANLEELQNRNRYTHILNVAEIDNFPERFTYANVRLWDESSAQLLPHWKETHRFIE 400
181 EMNANLEELQSGSDVYILNVTREIDNFPGLFAVHNIRVYDEETDILLAHWNEAYHFIN 240
401 AARQGTUHVLYCKKGVSSAATVLAAMKQECLEQALHVOELRPIARPNGFLROL 460
241 KAKNHSKCLVHCCKGVSSRSASTVLAAMKEFGWPLEKAYNYKQKXSTRPNAGFMROL 300
461 QIYOGILTASRQSH--VMEQKVGQ--VSPHEHPA-----PEVSTPF----- 497
301 SEVEGILDASKQRHNKLMWQOTDSSLQOPVDDPAGGDFLPETPDGPESQLPFLDDAQ 360
498 ----PPLP-----PEPGGEEKVYGMEE-----SOAPKEE---PGRPP 530
361 PGLGPPLPCCFRRSLDPLPSPEDETG--SLVHDEPEREALLLEAAPAEVHRPARQP 417
531 RINLRGVMRSISLLEPSL--ELESTSETDMPEVSSSHESHEEP 574
418 Q-----QSGGLCEKDVKKLEFPSPKGRSGSLQVETTEREGL 456

RESULT 14
US-09-955-732-15

Sequence 15, Application US/09955732
Publication No. US20020182203A1
GENERAL INFORMATION:
APPLICANT: Lucie, Ralf M.
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125,433
CURRENT APPLICATION NUMBER: US/09/955,732
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 552
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-732-15

Query Match 28.5%; Score 971; DB 10; Length 552;
Best Local Similarity 44.6%; Pred. No. 1,1e-68;
Matches 208; Conservative 73; Mismatches 121; Indels 64; Gaps 11;

163 LVLPLMSDTQVYLLDGDGFSVTSQGSRIFFKPIISIQTMWATLQVLAQCEALGSGLVPG 222
1 MVLRLMSDTKHLDDGDFSVSTAGRMHIFKPVSVQAWMSALQVLAHKAACEVARRHNYPG 60
223 GSALTWASHYQERLNSQSCINEMTAMADLESRLP--PSAEPGSSSQEQMEQAIRAEIM 280
61 GVALIMATVYSCISSEQSCINEMWAMQDLESTRPDSPLFVDKPTGEERTERLIKAKLR 120
281 KVLVSPDLESTYSKEIRQALELRGLPLQOYRDFIDNOMLLVLAQRASRIFFPLYLGS 340

121 SIMSODLENTYSKEIRNELEKQNNCNLKEKEFIDNEMLLIQMKPSLIFDLVLGS 180
341 EMNANLEELQNRNRYTHILNVAEIDNFPERFTYANVRLWDESSAQLLPHWKETHRFIE 400
181 EMNANLEELQSGSDVYILNVTREIDNFPGLFAVHNIRVYDEETDILLAHWNEAYHFIN 240
401 AARQGTUHVLYCKKGVSSAATVLAAMKQECLEQALHVOELRPIARPNGFLROL 460
241 KAKNHSKCLVHCCKGVSSRSASTVLAAMKEFGWPLEKAYNYKQKXSTRPNAGFMROL 300
461 QIYOGILTASRQSH--VMEQKVGQ--VSPHEHPA-----PEVSTPF----- 497
301 SEVEGILDASKQRHNKLMWQOTDSSLQOPVDDPAGGDFLPETPDGPESQLPFLDDAQ 360
498 ----PPLP-----PEPGGEEKVYGMEE-----SOAPKEE---PGRPP 530
361 PGLGPPLPCCFRRSLDPLPSPEDETG--SLVHDEPEREALLLEAAPAEVHRPARQP 417
531 RINLRGVMRSISLLEPSL--ELESTSETDMPEVSSSHESHEEP 574
418 Q-----QSGGLCEKDVKKLEFPSPKGRSGSLQVETTEREGL 456

RESULT 15
US-09-761-640-9

Sequence 9, Application US/09761640
Patent No. US20020137042A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: C1000964-CIP
CURRENT APPLICATION NUMBER: US/09/761,640
CURRENT FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 524
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-761-640-9

Query Match 26.9%; Score 918.5; DB 10; Length 524;
Best Local Similarity 37.9%; Pred. No. 1,6e-64;
Matches 205; Conservative 83; Mismatches 164; Indels 89; Gaps 7;

1 MALVTYSRSPPGSGA-STVGPWDAVQRRSRQKQSGFAVLRGAVLGQDGGDNDDAE 59
1 MALVTYQRPSPSVAGSCNSDGESEDEGNSKGNDRSECFAGGTALV----- 49
60 ASSEPTKAPSEBELGDDQDTDFQGSQSPQKQEGCRQHLVWQLRPDDIRLAAQLA 119
50 ALMDIPLPLOSERLSTDETRSSNSTOS--NNSDILHQMRYLLQREDTLKMAVKLS 107
120 PREPRLRYLVVS----- 132
108 QRSNRTRYLVIAASRCCSGSSTRRRRIRMRHNSVYKGSAGTKSSTSPAVPTQRLSYE 167
133 -----TREGGLS-----QDETVALGVDFPDSSSPSCTLGLVPLPMSD 170
168 QLTTEASSKDKTADENATAGDNKOTSGMESCLIGIDNERT-----TIGLVVILND 223
171 TOYLLDGDGFSVTSQGSRIFFKPIISIQTMWATLQVLAQCEALGSGLVPGSALTWAS 230
224 TTIHLDDGDFSVKYVEKTHIFKPVSVQAWMSALQVLAHKAACEVARRHNYPG 283
231 HYQERLNSQSCINEMTAMADLESRLPSPAEP--GSSSQEQMEQAIRAEIMKVLVSPDL 288
284 SYERRLESQSCINEMWAMQDLESTRPDSPLFVDKPTGEERTERLIKAKLR 343
289 ESYTSKEIRQALELRGLPLQOYRDFIDNOMLLVLAQRASRIFFPLYLGSWNAANE 348

Db 344 DEVTSKYIRGRLEBILDVLDGXYKSFIDAEMVLIGMDAPTKEHVVYLGSEWNASNLE 403
QY 349 ELQRRVTHHILNMAEILNPFYPERFTYNNVRLMDESAQLPHWKETHRFIEARAQGT 408
Db 404 ELQKRGVTHHILNVTREINFPFGTFRYNNRVYDEKTNLXWDDTFRYITRAKAEISK 463
QY 409 VLVHCKMGVSRSAATVLAAMKQYECSLQALRHVOELRPYRPNPGFLRQLOIYQILT 468
Db 464 VLVHCKMGVSRSAATVLAAMKQYECSLQALRHVOELRPYRPNPGFLRQLOIYQILT 523
QY 469 A 469
Db 524 A 524

Search completed: January 15, 2004, 06:55:08
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: January 15, 2004, 06:49:57 ; Search time 21 Seconds
(without alignments)
1327.755 Million cell updates/sec

Title: US-09-955-732-2

Perfect score: 3412
Sequence: 1 MLVTVSRSPGSGASTPVG.....FRKVVRAQASVHDSGHEGA 659

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1 | 239.5 | 7.0 | 482 | US-09-557-921-2 | Sequence 2, Appl1 |
| 2 | 237.5 | 7.0 | 172 | US-09-704-139-5 | Sequence 5, Appl1 |
| 3 | 234 | 6.9 | 173 | US-09-704-139-4 | Sequence 4, Appl1 |
| 4 | 232.5 | 6.8 | 397 | US-08-990-379-8 | Sequence 8, Appl1 |
| 5 | 219 | 6.4 | 170 | US-09-557-921-14 | Sequence 14, Appl1 |
| 6 | 219 | 6.4 | 171 | US-09-544-716-18 | Sequence 18, Appl1 |
| 7 | 219 | 6.4 | 171 | US-09-557-921-19 | Sequence 19, Appl1 |
| 8 | 218.5 | 6.4 | 784 | US-09-770-595A-3 | Sequence 3, Appl1 |
| 9 | 215.5 | 6.3 | 176 | US-09-704-139-2 | Sequence 2, Appl1 |
| 10 | 215.5 | 6.3 | 395 | US-08-990-379-5 | Sequence 5, Appl1 |
| 11 | 214 | 6.3 | 211 | US-09-544-716-2 | Sequence 2, Appl1 |
| 12 | 214 | 6.3 | 226 | US-09-045-973-8 | Sequence 8, Appl1 |
| 13 | 213.5 | 6.3 | 174 | US-09-544-716-20 | Sequence 20, Appl1 |
| 14 | 211.5 | 6.2 | 170 | US-09-544-716-14 | Sequence 14, Appl1 |
| 15 | 211.5 | 6.2 | 170 | US-09-557-921-15 | Sequence 15, Appl1 |
| 16 | 211 | 6.2 | 207 | US-09-013-881-4 | Sequence 4, Appl1 |
| 17 | 211 | 6.2 | 207 | US-09-612-473-4 | Sequence 4, Appl1 |
| 18 | 208.5 | 6.1 | 393 | US-08-990-379-4 | Sequence 4, Appl1 |
| 19 | 209 | 6.1 | 168 | US-09-544-716-15 | Sequence 15, Appl1 |
| 20 | 209 | 6.1 | 168 | US-09-557-921-16 | Sequence 16, Appl1 |
| 21 | 209 | 6.1 | 313 | US-08-990-379-7 | Sequence 7, Appl1 |
| 22 | 209 | 6.1 | 314 | US-09-164-193-22 | Sequence 22, Appl1 |
| 23 | 209 | 6.1 | 314 | US-09-221-448A-22 | Sequence 22, Appl1 |
| 24 | 206.5 | 6.1 | 394 | US-08-530-290-23 | Sequence 23, Appl1 |
| 25 | 206.5 | 6.1 | 394 | US-09-702-705-805 | Sequence 805, App |
| 26 | 206.5 | 6.1 | 394 | US-09-736-457-805 | Sequence 805, App |
| 27 | 206 | 6.0 | 661 | US-09-770-595A-22 | Sequence 22, Appl1 |

| | | | | | |
|----|-------|-----|-----|-------------------|--------------------|
| 28 | 205.5 | 6.0 | 394 | US-09-702-705-827 | Sequence 827, App |
| 29 | 205.5 | 6.0 | 394 | US-09-736-457-827 | Sequence 827, App |
| 30 | 204.5 | 6.0 | 302 | US-09-702-705-806 | Sequence 806, App |
| 31 | 204.5 | 6.0 | 302 | US-09-736-457-806 | Sequence 806, App |
| 32 | 203 | 5.9 | 169 | US-09-544-716-17 | Sequence 17, Appl1 |
| 33 | 203 | 5.9 | 169 | US-09-557-921-18 | Sequence 18, Appl1 |
| 34 | 202 | 5.9 | 169 | US-09-544-716-16 | Sequence 16, Appl1 |
| 35 | 202 | 5.9 | 169 | US-09-557-921-17 | Sequence 17, Appl1 |
| 36 | 202 | 5.9 | 367 | US-08-530-290-24 | Sequence 24, Appl1 |
| 37 | 200 | 5.9 | 263 | US-09-164-193-5 | Sequence 5, Appl1 |
| 38 | 200 | 5.9 | 263 | US-09-221-448A-5 | Sequence 2, Appl1 |
| 39 | 198.5 | 5.8 | 223 | US-09-685-853A-2 | Sequence 4, Appl1 |
| 40 | 196 | 5.7 | 87 | US-09-371-671B-4 | Sequence 11, Appl1 |
| 41 | 194 | 5.7 | 314 | US-09-371-671B-11 | Sequence 6, Appl1 |
| 42 | 194 | 5.7 | 367 | US-08-990-379-6 | Sequence 13, Appl1 |
| 43 | 193 | 5.7 | 168 | US-09-544-716-13 | Sequence 13, Appl1 |
| 44 | 193 | 5.7 | 168 | US-09-557-921-13 | Sequence 13, Appl1 |
| 45 | 191.5 | 5.6 | 353 | US-09-013-881-3 | Sequence 3, Appl1 |

ALIGNMENTS

RESULT 1
US-09-557-921-2
; Sequence 2, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-2

Query Match 7.0%; Score 239.5; DB 4; Length 482;
Best Local Similarity 28.0%; Pred. No. 2.5e-13;
Matches 73; Conservative 44; Mismatches 117; Indels 27; Gaps 6;

| | | |
|----|-----|---|
| QY | 232 | YQRLNSESQSCINENTMADLESLRPPSAEP-----GSSSEQEQMCAT---RAELMKYLD 284 |
| DB | 236 | YDENTNEPRVMPQPLHIVLSLREKGEPLVKQGLSSFFQNHENLQDNLQLOECRE 295 |
| QY | 285 | VSDLESVTSKELRQALELRGLPLOQYRDFIDNOMLLVAQRDRASRIFFPHLYLSEWNA 344 |
| DB | 296 | VGGGAASASLPLQ-----PIPTPD-ENNEL-----TPIPLPFLGNEQDA 337 |
| QY | 345 | ANIEELQNRVTHILNMAEINDFPER--FYHVRVLDSESAQLPIMKETHPIENA 402 |
| DB | 338 | ODIDTQRLNIGGVIVNTHTLPLVHYEKLFFYKRLPADDSKNQKRIQYFEAFETEEA 397 |
| QY | 403 | RAGCTVVLVHCKVGRSAATVLAAMKQYESLLEQALHVOELPIRAPNGFLRQLOI 462 |
| DB | 398 | HQCGKGLLHCQGVRSATIVIAIYIMKTRMTMDAYFVAGKRIIISPNLPMQQLLE 457 |
| QY | 463 | YQGITASRQSHWEQKGV 483 |
| DB | 458 | FEEDLNNGVTRILTPKMGV 478 |

RESULT 2
US-09-704-139-5
; Sequence 5, Application US/09704139
; Patent No. 6420153
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosanna

TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
 FILE REFERENCE: 10448-018001
 CURRENT APPLICATION NUMBER: US/09/704,139
 CURRENT FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: US 60/185,772
 PRIOR FILING DATE: 2000-02-29
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patent version 3.0
 SEQ ID NO 5
 LENGTH: 172
 TYPE: PRT
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(172)
 OTHER INFORMATION: consensus sequence
 US-09-704-139-5

Query Match 7.0%; Score 237.5; DB 4; Length 172;
 Best Local Similarity 37.9%; Pred. No. 6.8e-14;
 Matches 64; Conservative 23; Mismatches 47; Indels 35; Gaps 7;

QY 330 SRIFPHYLGESEWNA--ANLEELQNRVTHILNMAREI-----DNFYPER----- 372
 DB 3 SEILPHYLGSYDASEANLALKKLGITHIVNTEEVNPNFELKKQDRYTYNEYSKG 62
 QY 373 --FTYHNVR-----LMDESAQLLPKMKETHRPIEARAQGTHVYHCKMGVSRSA 421
 DB 63 SGFTYLOIPNVDDIYHIAMNTER-KISKYLEAVEVEFLEDEKKGGCVLVHCCQAGVSRSA 121
 QY 422 ATVLAYAMKQYECSELEQA-----LRHVOELR-PIARPENGFRLQLOIYQ 464
 DB 122 TLVLAIVLMTKTNLSLRDAYDFVYVYHIKERCPILISNFGRLRIEYE 170

RESULT 3
 US-09-704-139-4
 Sequence 4, Application US/09704139
 Patent No. 6420153
 GENERAL INFORMATION:
 APPLICANT: Kapellier, Rosanna
 TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
 FILE REFERENCE: 10448-018001
 CURRENT APPLICATION NUMBER: US/09/704,139
 CURRENT FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: US 60/185,772
 PRIOR FILING DATE: 2000-02-29
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patent version 3.0
 SEQ ID NO 4
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(173)
 OTHER INFORMATION: consensus sequence
 US-09-704-139-4

Query Match 6.9%; Score 234; DB 4; Length 173;
 Best Local Similarity 35.9%; Pred. No. 1.4e-11;
 Matches 61; Conservative 26; Mismatches 47; Indels 36; Gaps 6;
 QY 330 SRIFPHYLGESEWNA--ANLEELQNRVTHILNMAREIDNYP----- 370
 DB 3 SEILPHYLGSYDASEANLALKKLGITHIVNTEEVNPNFELKKQDRYTYNAYISKV 62
 QY 371 ERFYHNVR-----LMDESAQLLPKMKETHRPIEARAQGTHVYHCKMGVSRSA 420
 DB 63 SGFTYLOIPNVDDIYHIAMNTER-KISKYFDEAVDFIDDAKQGGKVLVHCCQAGISBS 121
 QY 421 AATLAVAMKQYECSELEQA-----LRHVOELR-PIARPENGFRLQLOIYQ 464

DB 122 AATLAVAMKTNLSLNEAYDFVYVYHIKERCPILISNFGRLRIEYE 171
 RESULT 4
 US-08-990-379-8
 Sequence 8, Application US/08990379
 Patent No. 5998188
 GENERAL INFORMATION:
 APPLICANT: Stork, Philip J
 TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cdnas and
 TITLE OF INVENTION: Theor Biologically Active Expression Products
 FILE REFERENCE: 4104-000322US
 CURRENT APPLICATION NUMBER: US/08/990,379
 CURRENT FILING DATE: 1997-12-15
 EARLIER APPLICATION NUMBER: PCT/US96/10402
 EARLIER FILING DATE: 1996-06-14
 EARLIER APPLICATION NUMBER: 60/000,263
 EARLIER FILING DATE: 1995-06-16
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 8
 LENGTH: 397
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-990-379-8

Query Match 6.8%; Score 232.5; DB 2; Length 397;
 Best Local Similarity 27.8%; Pred. No. 7.8e-13;
 Matches 74; Conservative 49; Mismatches 106; Indels 37; Gaps 9;

QY 287 DLEVTSKEI--ROALELRLGLPL--QQYRPFIDNQMLLVAQRDRASRIFPHYLGESEW 342
 DB 141 DVKPIQSEKIESERLILQCGKPVNVSVYRPAYD-----QGGVEILLPFLYLSAY 191
 QY 343 NANLEELQNRVTHILNMAREIDNYPERTYHNVRLMDESAQLLPKMKETHRPIEARA 402
 DB 192 HASKCEPLANLHITALVNSRSTSEACWTHLYKMIPEVDSHTADISSHFOEALDFIDCV 251
 QY 403 RAQGTHVYHCKMGVSRSAATVLAYAMKQYECSELEQALRHVOELRPIARPENGFRLQOI 462
 DB 252 RKSGKVLVHCEAGISRSPTTCMAVLMKTKQRLKEADYIKQRSWVSNFGFWGLQLQ 311
 QY 463 YQGIH---TASROSHWQEKVGVSPFEH---PAPEVS---TPPP-----LPPEBGG 507
 DB 312 YESILPSTPNQPPSCGGEAAGSLLGHLDTLSPDQGAICTPSPASVLAACLPFGQSQS 371
 QY 508 GEEKY-----VGMESQAAPKEE 525
 DB 372 SAELMQRPNPAKTGMES--AQPOEQ 396

RESULT 5
 US-09-557-921-14
 Sequence 14, Application US/09557921
 Patent No. 6551810
 GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125,416
 CURRENT APPLICATION NUMBER: US/09/557,921
 CURRENT FILING DATE: 2000-04-20
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 170
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-557-921-14

Query Match 6.4%; Score 219; DB 4; Length 170;
 Best Local Similarity 35.1%; Pred. No. 3.4e-12;

[illegible]

```

RESULT 6
US-09-544-716-18
: Sequence 18, Application US/09544716
: Patent No. 6492157
: GENERAL INFORMATION:
: APPLICANT: Lucide, Ralf M.
: APPLICANT: Wei, Bo
: TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
: FILE REFERENCE: 200125.415
: CURRENT APPLICATION NUMBER: US/09/544,716
: CURRENT FILING DATE: 2000-04-10
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 18
: LENGTH: 171
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-544-716-18

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| | Query Match | 6.48 | Score 219 | DB 4 | Length 171 | |
|----|-----------------------|--|------------------|----------|------------|--|
| | Best Local Similarity | 33.8% | Pred No. 3.4e-12 | | | |
| | Matches 47 | Conservative 29 | Mismatches 63 | Indels 0 | Gaps 0 | |
| QY | 332 | IPEHLVIGSEWNANLEELORNRVTHTLNMAAEIDNFPERTYHNVRLWDESAQLHP | 391 | | | |
| Dd | 30 | ILFLVLGVYSKSCPELANLHTALTNLSRSTSEAOMTHLYKWLPVEDSHTDIISB | 89 | | | |
| QY | 392 | WKETHRFIEARAQGHIVLVCKMGVSASATVLAIVANKQYESGLQALHNVDLPPIAR | 451 | | | |
| Dd | 90 | FQEAIFIDICVERKGKVLTWEAGSISPITCMAYLMKTQFPLKEAFDYIKORSMS | 149 | | | |
| QY | 452 | PNPGFLROLQIYGIIITAS | 470 | | | |
| Dd | 150 | PNFGFMGLLIQYBSILPS | 168 | | | |

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RESULT 7
US-09-557-921-19
: Sequence 19, Application US/0957921
: Patent No. 6551810
: GENERAL INFORMATION:
: APPLICANT: LucHe, Ralf M.
: APPLICANT: Wei, Bo
: TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
: FILE REFERENCE: 200125.416
: CURRENT APPLICATION NUMBER: US/09/557,921
: CURRENT FILING DATE: 2000-04-20
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO. 19
: LENGTH: 171
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-557-921-19

```

```

Query Match: 6.4%; Score 219; DB: 4; Length 171;
Best Local Similarity: 33.8%; Pred: No. 3.4e-12;
Matches 47; Conservative 29; Mismatches 63; Indels 0; Gaps 0

```

```

QY 332 IEPHVLTSGENAANLDEELQNRVRVTHLNMAREIDNFPPEEFTYHVRMLNMEESAGCLPH 391
    " 30 ILEFVLTSAYHNSKCEPLANHLITALLNVSFRFSEACMTHLYKMTPVEDSHIADLSSH 89
QY 392 WKRETRFRIBARACQHTVILVHCXMGVSSRAATVLAAMKQYECSELOALRHVCELRIPAR 451
    " 30 FQALPFDIOVAREKKGKTVIVHCEAGISRPITCAALYMKTKQFRLKEAFDITKQRBGMVS 149
Db 90 FQALPFDIOVAREKKGKTVIVHCEAGISRPITCAALYMKTKQFRLKEAFDITKQRBGMVS 149
QY 452 PNEGFLRLOIYQGIINTAS 470
    " 30 PNEGFLRLOIYQGIINTAS 150
Db 150 PNEGFLRLOIYQGIINTAS 150

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RESULT 8
US-09-770-595A-3
; Sequence 3, Application US/09770595A
; Patent No. 6566511
; GENERAL INFORMATION:
; APPLICANT: Revencova, Ekaterina
; APPLICANT: Razzkovski, Jurek
; TITLE OF INVENTION: Map Kinase Phosphatase Mutant
; FILE REFERENCE: S-30589A
; CURRENT APPLICATION NUMBER: US/09/770,595A
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentVer 2.1
; SEQ ID NO 3
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-770-595A-3

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| Query Match | Score | DB | Length |
|------------------------------|-----------------|-------------------|-----------------|
| Query Match Similarity 25.5% | 6.4% | Score 218.5 | DB 4 Length 784 |
| Best Local Similarity | 5.5% | Pred. No. 4,7e-11 | |
| Matches 80 | Conservative 48 | Mismatches 137 | Indels 49 |
| | | | Gaps 9 |

RESULT 9
US-09-704-139-2
Sequence 2, Application US/09704139
Patent No. 6420153
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosanna
TITLE OR INVENTION: 18232 A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
FILE REFERENCE: 10448-018001
CURRENT APPLICATION NUMBER: US/09/704,139
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/185,772

PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1390)
OTHER INFORMATION: n = a, t, g, or c
US-09-704-139-2

Query Match 6.3% Score 215.5; DB 4; Length 176;
Best Local Similarity 38.9% Pred. No. 7.5e-12;
Matches 61; Conservative 22; Mismatches 71; Indels 3; Gaps 2;

QY 331 RIFPHLYGSEMNANIEELQNRVTHILNMAREIDNPFYERFTHNVRLMDEBSAQILP 330
DB 21 RFAISLFIQSARAAAGAEQLRAGVTLICVNSRQPGPRAPGVAEVLVPPFDPAEDLLA 80
QY 391 HWKETHREIAPAAQGHVHVCHCKGVSRSAATVLAAMKQYECSEQLRHYQELRPIA 450
DB 81 HLEPTCAMEAFAVAGGACLVYCKGRSRSAVCTAYIMRHRGLSLAKAQMYKSAPVA 140
QY 451 RPNPGFLRQLQYQOILFASRQSHV-WEQKVGVGPSPE 486
DB 141 EPNPGFMSQLQKTEBALQ--QSCLOGEPFALGSPF 175

RESULT 10
US-08-990-379-5
Sequence 5, Application US/08990379
Patent No. 5998188

GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Mistra-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
FILE REFERENCE: 4104-000322USA
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,263
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 395
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-990-379-5

Query Match 6.3% Score 215.5; DB 2; Length 395;
Best Local Similarity 22.7% Pred. No. 2.8e-11;
Matches 87; Conservative 54; Mismatches 130; Indels 113; Gaps 10;

QY 176 DGDGFSVTSQSGQRIFRPTISIQTMATLQVHQACEALGSLVPGSALTW----- 228
DB 22 DENGSTAGSSGGS-----HGAL-----GLSSGKCLLLDCRPFLLA 56
QY 229 --ASHYQERLNSQSCINEMTA--MADLESIRPPSAFPGSSSEBQEQAIRLELWKYLD 284
DB 57 HSAGYIRGSVNVNRCNTIVRRRAKGSVSLQILP-----AEEVFRARLSGLYSAVI 107
QY 285 VSDLESVTSKEIRQALEIRLGLPQOYRDFID-NQMLLLVAQRDRA----- 330
DB 108 VYDERSRRAESLR--DSYSLVVLQALRRNAERDILLGQYERFSESEYPERCSKTKAL 165
QY 331 -----RIFPHLYGSEMNANIEELQNRVTH 357
DB 166 AAIIPPVPPTNESLIDGSCSGTPLHDGQGVAILPFLYIGSAVHAARDMDALGITA 225

QY 358 ILMNAREIDNPFYERFTHNVRLMDEBSAQILPHMKETHREIAPAAQGHVHVCHCKGV 417
DB 226 LINVSSDCNHFEGYQYKCIPEVDNHRKADISSWFEAIEYLDVAKDGRGVLVHCQAGI 285
QY 418 SRSAATVLAAMKQYECSEQLRHYQELRPIARENPFELRQ-LQIYQGITFASRQSHV 476
DB 286 SRSAITCLAYIMMKRVLEEFVYKORRSLISNFSFMOLLQFESQVITLS----- 339
QY 477 EOKVGVSPDEHPAPEVSTPPPL 500
DB 340 -----CAEAASPSGFL 351

RESULT 11
US-09-544-716-2
Sequence 2, Application US/09544716
Patent No. 6492157

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.415
CURRENT APPLICATION NUMBER: US/09/544,716
CURRENT FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapiens
US-09-544-716-2

Query Match 6.3% Score 214; DB 4; Length 211;
Best Local Similarity 37.1% Pred. No. 1.4e-11;
Matches 56; Conservative 26; Mismatches 57; Indels 12; Gaps 4;

QY 327 DEASRIFPHLYGSEMNANIEELQNRVTHILNMAREIDNPFYERF-----THNVFLM 381
DB 60 HNADRWPGLYIGDQDMNNRRLRLGITVNLASHSRMRGTGEAYEGIGIRYIGVAAH 119
QY 382 DEBSAQILPHMKETHREIAPAAQ-GTHVHVCHCKGVSRSAATVLAAMKQYECSEQLRQAL 440
DB 120 DSPAFDWSIHFOYADFIHRLISQPGKILVHCAGVSRSAITVLAYIMLHYHLLTVBAI 179
QY 441 RHVQELRPIARENPFELRQ-----QIYQGI 466
DB 180 KVKXDRGII-ENRGEFLRQLALDRRLRQGL 209

RESULT 12
US-09-045-973-8
Sequence 8, Application US/09045973
Patent No. 6165767

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Giegler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

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1 SOFTWARE: FastSeq for Windows Version 2.0
2
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/045,973
5 FILING DATE: Filed Herewith
6
7 CLASSIFICATION:
8
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER:
11 FILING DATE:
12
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Billings, Lucy J.
15 REGISTRATION NUMBER: 36,749
16 REFERENCE/DOCKET NUMBER: PF-0491 US
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (650) 855-0555
19 TELEFAX: (650) 845-4166
20
21 TELEX:
22
23 INFORMATION FOR SEQ ID NO: 8:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 226 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 IMMEDIATE SOURCE:
31 LIBRARY: GenBank
32 CLONE: 1495338
33
34 US-09-045-973-8

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|-----------------------|--------|--|--------|----------------|
| Query Match | 6.3%; | Score 214; | DB 3; | Length 226; |
| Best Local Similarity | 29.7%; | Pred. No. 1,6e-11; | | |
| Matches | 69; | Conservative | 40; | Mismatches 87; |
| | | | Indels | 36; |
| | | | Gaps | 10; |
| QY | 330 | SRIPPHLYLGESEWNAANLEELORNFVTHILNMAKEIDNFYPERFFYHNNRLWDESSAQ--- | 387 | |
| Db | 15 | SEIVPGLTICGV-SALSKDEMKEKHKITHIINNTTVPNI-RSLGDIORTKLTLEETPOTY | 72 | |
| QY | 388 | LLPHWKEHTRFEAPAAQGTHTVLYHCKKGVSSAATVAYAMKQYEC-SLEQALHVOEL | 446 | |
| Db | 73 | IYPHLELSDQIQALINAGGKTVLCVAVGSNSPACICLAFILK-YRCNLRRAHYLMMSK | 131 | |
| QY | 447 | KPIAPENFGFLRQLOIYQGILTASRQSHWEQKVGCV-----SPEE-HPADEVSTPEP | 498 | |
| Db | 132 | RSMTVEPNLGFQROLIAYEQNV-----KENAGSVTLVRDEAQPEQLLPVYVNIINAIIP | 182 | |
| QY | 499 | PLPEPEEGGEKGVVMESSQAAPKEPQGPRIIRLQGMRSISLLEPSLEL | 550 | |
| Db | 183 | ARPSAPF-----QDPNMIDPE--PRRRNSGFKSKRPVLPPEVMEH | 221 | |

```

RESULT 13
US-09-544-716-20
; Sequence 20, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Lucne, Ralf M.
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-20

```

```

Query Match      6.3%; Score 213.5; DB 4; Length 174;
Best Local Similarity 38.6%; Pred. No. 1.1e-11;
Matches 54; Conservative 23; Mismatches 56; Indels 7; Gaps 3

QY 327 DRASLIFPLVLIGSEMANALEEQNRVTHLLNARELDNYPYRF-----TYHNKVLW 381
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

| | | | |
|----|-----|---|-----|
| Db | 27 | NHAEDEWPGVLYGDQDMANNRELRILGITVHLNLSHSMRGTEPAEGGIRILGYEAH | 86 |
| Qy | 382 | DESAQQLDPHKKEHTFEIEAARQ-GTVLVNCHCKGVSRSAATVLAAMKQVECSLQAL | 440 |
| Db | 87 | DSAPFMSTHFGPAADFIRALSSQGGKILVHCAGVSRATLVLAIVMLVHHTLVEAI | 146 |
| Qy | 441 | RHYQELRLPIARPMPSGLRQL | 460 |
| Db | 147 | KVYKDKRGIT-PRRGFLRQL | 165 |

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RESULT 14
US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
;
; APPLICANT: Rei, Bo
;
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-14

```

| | Query March | 6.2% | Score 211.5; | DB 4; | Length 170; |
|----|-----------------------|--|-----------------------|-----------|-------------|
| | Best Local Similarity | 36.2% | Pred 21.6-11; | | |
| | Matches 51; | Conservative 24; | Mismatches 61; | Indels 5; | Gaps 2 |
| Cy | 330 | SRIFPHLYGSEWNANLEELQRNVTILNMAREI--- | DNFYPERFTYHNVRIMDEESA | 386 | |
| Db | 28 | TRILPHLYGSDVDVKNLDMTONGISVLANASNCPPKDFICESRFM-- | RVPIINDVYCE | 85 | |
| Cy | 387 | QLIPHKETRRFFEARPAQGTAVLVHCKKGVRSNATVLAAMQYBESJLEQALRHQEL | 444 | | |
| Db | 86 | KLIPWLDKRSLEPFDKDKLSSCCVIVYHCLAGISRSRTIAIAIYIMTMGNSDDAAYRFVKDR | 145 | | |
| Cy | 447 | RPIARPDPGLRLOQLYQGITL | 467 | | |
| Db | 146 | RPSISEVNFPLGQLLEYERKL | 166 | | |

```

RESULT 15
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-15

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Query Match      6.2%; Score 211.5; DB 4; Length 170;
Query Similarity 36.2%; Pred No. 1.6e-11;
Best Local      51; Conservative 24; Mismatches 61; Indels 5; Gaps 2
Matches
Qy      330  SRIFPHLYGSEWNAANLEEDRNRYTHILINKAREI---DNFYPERFTHENVIRIMDESA 368
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      28    TRILPHLYGSCQDVLINKDLMTONGISVYLNASNSCPKPDTCESRF--RVPIINDNCE 85

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